

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 01:57:11 ; Search time 5413.87 Seconds
(without alignments)
9562.892 Million cell updates/sec

Title: US-09-763-957-3
Perfect score: 2474
Sequence: 1 ttacagatacacagaatcag.....taaccacatacacacatatgg 2474

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htgo.inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

C	1	147.4	5.0	86827	3	PFMAL3P5	AL034556 Plasmodiu
C	2	144.4	5.8	67970	3	PFMAL1P3	AL031746 Plasmodiu
C	3	144.4	5.8	172816	3	AC093899	AC093899 Homo sapi
C	4	143.6	5.8	4601	3	DMU1584	U1584 Drosophila
C	5	143.6	5.8	19517	3	DMU37541	U37541 Drosophila
C	6	142.6	5.8	159618	9	AC096750	AC096750 Homo sapi
C	7	141.4	5.7	172724	2	AC098590	AC098590 Homo sapi
C	8	140.8	5.7	159618	9	AC096750	AC096750 Homo sapi
C	9	138.2	5.6	67970	3	PFMAL1P3	AL031746 Plasmodiu
C	10	137.8	5.6	168698	9	AC068138	AC068138 Homo sapi
C	11	136.8	5.5	349980	6	AX344555	AX344555 Sequence
C	12	136.6	5.5	14867	3	AE001398	AE001398 Plasmodiu
C	13	136.6	5.5	104992	2	AC005504	AC005504 Plasmodiu
C	14	136.6	5.5	169546	2	AC004157	AC004157 Plasmodiu
C	15	136.4	5.5	104992	2	AC005504	AC005504 Plasmodiu
C	16	136.4	5.5	169546	2	AC004157	AC004157 Plasmodiu
C	17	136.2	5.5	155106	2	AC104069	AC104069 Homo sapi
C	18	136.2	5.5	326924	2	AC093082	AC093082 Homo sapi
C	19	135	5.5	181792	2	AC098822	AC098822 Homo sapi
C	20	134.2	5.4	205130	2	AC105425	AC105425 Homo sapi
C	21	133.6	5.4	155106	2	AC104069	AC104069 Homo sapi
C	22	133.4	5.4	246080	2	AC104073	AC104073 Homo sapi
C	23	133.2	5.4	168698	9	AC068138	AC068138 Homo sapi
C	24	133	5.4	181792	2	AC098822	AC098822 Homo sapi
C	25	132	5.3	172724	2	AC098590	AC098590 Homo sapi
C	26	132	5.3	326924	2	AC093082	AC093082 Homo sapi
C	27	131	5.3	130117	9	AC004907	AC004907 Homo sapi
C	28	131	5.3	158398	2	AC011146	AC011146 Homo sapi
C	29	130.4	5.3	14867	3	AE001398	AE001398 Plasmodiu
C	30	130.2	5.3	205130	2	AC105425	AC105425 Homo sapi
C	31	130	5.3	86827	3	PFMAL3P5	AL034556 Plasmodiu
C	32	129.6	5.2	349980	6	AX344555	AX344555 Sequence
C	33	129.2	5.2	136357	2	AL161942	AL161942 Homo sapi
C	34	129	5.2	183584	9	AC012492	AC012492 Homo sapi
C	35	128.8	5.2	137889	9	AC073269	AC073269 Homo sapi
C	36	128.4	5.2	15421	3	PFCOMPIRA	X95275 P. falciparu
C	37	127.6	5.2	183584	9	AC012492	AC012492 Homo sapi
C	38	127	5.1	101188	2	AC010606	AC010606 Homo sapi
C	39	127	5.1	184838	9	AC090740	AC090740 Homo sapi
C	40	126.8	5.1	152209	9	HS1108D11	AL034419 Human DNA
C	41	126.6	5.1	136098	9	AC006970	AC006970 Homo sapi
C	42	126.6	5.1	152209	9	HS1108D11	AL034419 Human DNA
C	43	126.4	5.1	246080	2	AC104073	AC104073 Homo sapi
C	44	126.2	5.1	135250	9	AC104320	AC104320 Homo sapi
C	45	126.2	5.1	136098	9	AC006970	AC006970 Homo sapi

ALIGNMENTS

RESULT 1
PFMAL3P5/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

PFMAL3P5 86827 bp DNA linear INV 04-MAY-2000
Plasmodium falciparum MAL3P5, complete sequence
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179

AL034556.3 GI:7711064

HTG; centromere; CTRP protein; initiation factor E4;

Serine/threonine protein phosphatase.

Plasmodium falciparum

Eukaryota; Alveolata;

1 (bases 1 to 86827)

Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T.,

Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,

Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,

Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J.,

Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A.,

Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S.,

Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and

Barrell, B.G.

The complete nucleotide sequence of chromosome 3 of Plasmodium

falciparum

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Query Match 6.0%; Score 147.4; DB 3; Length 86827;
Best Local Similarity 45.7%; Pred. No. 6.7e-11;
Matches 659; Conservative 0; Mismatches 776; Indels 6; Gaps 4;
QY 564 taactaagggcccaacttaccctttataatctctcctcaactcgggttttggaagtac 623
DB 40358 TAAATAAATAAATATATATATTAATAATAATAATAATAATAATAATAATAAAT 40299
QY 624 aactttctactcttatttaagggaggtattttttccatataccaaattaatttttt 683
DB 40298 AAAATTAAAT 40239
QY 684 tttaattatgcatttggctcttataataaacaattatggtatggttaagtcgtatat 743
DB 40238 TAAATTAATTAACAGATTTAATAATACGTCGTGTAATATATATATATATATAT 40179
QY 744 cggtagcaattgaagtttctcctcaagtttagccatttttatgaaattaaacttaact 803
DB 40178 TTATTTTAATATGTATTCATTAATAATAATAATAATAATAATAATAATAATAAT 40119
QY 804 actattaggttaactatgatcatcaaatccaatttcaatgaggttcaattttaccocaa 863
DB 40118 AAAAATACTAT 40059
QY 864 gattgaaagtgtgttgcaacttcgttcaactaaagtgtgattataaggttgacgacttt 923
DB 40058 AAAATAAATAAATGAT 39999
QY 924 aacctaaatttttgaattgaaggggttgatgacttcagcttcaaaataaattcaacta 983
DB 39998 AAATTATTATTAAGTAAACATTTAATTTAATTTAAATTTAATTTAATTTAATTTA 39939
QY 984 aagttctagactacattggagatttttagtttcataaaattttgagaaaaggctgaacta 1043
DB 39938 TTAAGAATTAAAT 39879
QY 1044 aagttatgaaaaagattgggactattcaattcaattagttgtgaattgatgacaaattt 1103
DB 39878 TAAATTAATTAATTTTAAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTT 39819

QY 1104 tcatgacataaccacatcagagaaataccacctcgacgactacacaaatctcaatgta 1163
DB 39818 AAGTGGAAATAAATAAATAAATTTATTTATTTATTTATTTATTTATTTATTTATTT 39759
QY 1164 attaatgaagcattgtagtataagagctcagaataaattcttcaaatattagagga 1223
DB 39758 CTTATTTAAATTCATTTAAATTAATATATATATATATATTTGAATTTAATTTATTT 39699
QY 1224 ctatttttaaaaaattcaagaaagtttgatctataacccttttaaacctttaaatc 1283
DB 39698 ATAAATTTAAATTAATAAATAAATTTATTTATTTAAATTTAATTTAATTTAATTTA 39639
QY 1284 taacaaattttctttagactcacattgtgtgtagaggggtgatttctcaaaatatat 1343
DB 39638 TTATATAATATATTTATTTGAATTTAATTTATTTATTTATTTATTTAATTTAATAT 39579
QY 1344 atttttactagtagtattgtctgcgaattatataatagttatttaacttgggaaatg 1403
DB 39578 ATATTAATTTATTTATTTAATTTAATTTATTTATTTATTTAATTTAATTTAATTTA 39519
QY 1404 gcctaaataagttataaaaaaggagaaaattatttattcataaaaaaaacacacctaa 1463
DB 39518 AATTTATTTATTTAATTTAATTTATTTATTTAATTTAATTTAATTTAATTTAATTTA 39459
QY 1464 gtaacaataataaaaaacattatataagagattaaagataatttttaagttattgaa 1523
DB 39458 TTTTTTATTTAATAAATAAATAAATAAATTTATTTATTTTAAATAAATAAATAAATA 39399
QY 1524 gaataattttttattataaaatttgaactaaaaataatccaaataatcaaaagtaaa 1583
DB 39398 AATTTATTTTATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 39340
QY 1584 agataataatcatcattcaatacacagtaacagtaacattcatatacatatattagata 1643
DB 39339 ATATATAATTTATTTTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAA 39280
QY 1644 tatacaaatatttggtttaaattttacattattattactaaataatataattttctttg 1703
DB 39279 AATATATATATTAATTTATTTTATTTTAAATAAATAAATAAATAAATAAATAA 39221
QY 1704 aatatctttttatacaagtaggtagactagaagaattattcttattctcccgataatt 1763
DB 39220 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 39163
QY 1764 atgttaaatgttaacggcgttagactgattttgttgcattattattataaataatc 1823
DB 39162 ATTTTATTTTAAATATATATATATATATATTTATTTATTTATTTATTTATTTA 39105
QY 1824 gagatttaagttaatgtctctcttcttgcatttttaacatgggtctcaaaaattagg 1883
DB 39104 TAAATTAATATATATATATATAACATTTACATATATTTTATTTTATTTTATTTA 39045
QY 1884 ttgcgtcctcaatgaacccatgctatattgttttaagttttttgttttttgacaattgt 1943
DB 39044 TTATTTTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 38985
QY 1944 ttctattctgcagattgctcttaggattgaaattattgttgcatactagaacgaaga 2003
DB 38984 GTAAATTAATTAATAAATAAATGTTATCAATATTAATTAATAAATAAATAAATA 38925
QY 2004 a 2004
DB 38924 A 38924

RESULT 2

PFMAL1P3

LOCUS

DEFINITION Plasmodium falciparum MALLP3, complete sequence.

ACCESSION AL031746

VERSION AL031746.9 GI:6594243

KEYWORDS HTG.

PFMAL1P3

Plasmodium falciparum MALLP3, complete sequence.

AL031746

AL031746.9 GI:6594243

HTG.

67970 bp

DNA linear

INV 15-DEC-1999

[illegible]


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/db_xref="GI:6594248"
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CFNYSIDSLAGSSKSEKVKVDIPNIELKSLNINYEYKMKKIEVGFSDMNNLN
IANEVLKHTSTNIEFSLINDSSKSPVLTFLKEFGSIFPHMLNNYFKLLFDLCQ
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36744..36749
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Best Local Similarity 48.3%; Pred. No. 1.7e-10;
Matches 663; Conservative 0; Mismatches 681; Indels 30; Gaps 8;

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QY 699 ttgatctattataaacaatttgatggattgaagtcgtatcggtgacaattgaag 758
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DB 8449 ATATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8508
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QY 759 ttttcctcaagtttagccattttttatgaattaaaccttaactactactattaggtaaatt 818
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QY 819 catatgataccaatttcgaattgagtttcaattttaccagaatttggaagtgttt 878
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QY 879 gtcaactctgttaactaaagttgtattataaggttgacgacctttaacctaaatctattt 938
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QY 989 ctgactacactggagatttaggttcataaaatttttagaaaaaggctgagttcaagt- 1047
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DB 8749 TTTAAATATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8808
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QY 1048 ---tatgaaaaaagattggtgactattccaatttaattgttggaattgatgacaaat-att 1103
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DB 8809 TTATATTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8868
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QY 1104 tcatgagcataccaactcagagaataaccacctgcgacgactacaacaactcgaattgta 1163
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QY 1164 attaaatgaagcattgtagtaagagctcagaaataatttcttaataatttagaggaa-a 1222
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DB 8929 AATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8988
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QY 1223 actatttttaaaaaattacaagaagaatttgatctataaacctctttaaacctttaaatat 1282
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QY 1283 ctaacaattttcttatgactcacacattggttgatgaggtgattttgtcaaaaatatgtc 1342
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QY 1343 tattttatactagtagtattgtgtcgcgaattatatactagatttaaccttggagaaatgat 1402
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QY 1452 acacttaataagtaacaataataaaaaacattataataagagattaagataaatttaataa 1511
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QY 1571 caaagtaataatagatataatcatcatcaatcacgagtaaatcaatcattattataatca 1630
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QY 1690 tattaatttttgaatacatcttttatacaagtgaggtagacagagaattatctatctctc 1749
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QY 1750 ccgtattttgtgagattgaagaatgaacggcttagactgatttttctgtattatattat 1809
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DB 9529 ATATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9588
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QY 1810 ttataaatccattagagatttaagtttaagtctctctc-ttgatttttaaacatgggtctcaaa 1868
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DB 9589 TTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9648
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QY 1869 aattaggttttaactaatgogtccatgaacccatgctatatgtttttaagaattttttgt 1928
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DB 9649 TAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9708
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QY 1929 tttttgacaagtgttttttttttttttttttttttttttttttttttttttttttttttt 1982
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DB 9709 ATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9762
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RESULT 3
AC093899      172816 bp      DNA      linear      PRI 05-FEB-2002
DEFINITION    Homo sapiens chromosome 2 clone RP11-724O16, complete sequence.
ACCESSION     AC093899 AC068884
VERSION       AC093899.3 GI:18497265
KEYWORDS      HTG.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 172816)
AUTHORS      Waterston,R.H.
TITLE        The sequence of Homo sapiens clone
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 172816)
AUTHORS      Waterston,R.H.
TITLE        Direct Submision
JOURNAL       Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE     3 (bases 1 to 172816)
AUTHORS      Waterston,R.H.
TITLE        Direct Submision
JOURNAL       Submitted (05-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT       On Feb 5, 2002 this sequence version replaced gi:15625013.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_NH0724O16
Drafting center: WIBR
----- Location/Qualifiers -----
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BASE COUNT    53405 a 33788 c 33104 g 52519 t
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Query Match      5.8%; Score 144.4; DB 9; Length 172816;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 653; Conservative 0; Mismatches 696; Indels 21; Gaps 7;

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DB 22801 TTTTAATATATATTATATAAATATATTTTATATATAAATATATATTTAATATAAATATCTT 22860

QY 688 atttatgaatttgatcttatataaacaattatggatggatttaagtcgtatcgggt 747
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DB 22861 TATATTTAATATATATTTAATATAAATATCTTTATTTAATATATATTTATATATAAAT 22920

QY 748 gcaattgaaagtttccccaagtttagccatttttatgaaaataaacttaacacta 807
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DB 22921 -ATATATTATATTTAATATATTTAATTTAATATACGGTTATTTAATATATATTTT 22979

QY 808 ttaggtaaatcatatgatcatttaacaatttcaattgagttcatttttaaccaagatt 867
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DB 22980 CTATATAAATATATTTATATTAACATATATTTATATATAAATATATTTATATATTAATA 23039

QY 868 tgaagttgttgcaactctctgttaactaaagttgtattataaaggttgacgacttaacc 927
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DB 23040 TTTACATATAAATATATTTATATGATGATATTTTACATATAAATATATTTATATTTAATA 23099

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QY 928 taaatctattttgaaattgaaggggttgatgacttcagcttttaaaaaataaactcaaaagt 987
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QY 988 tctagacacattggagagatttttagtgttcataaaaaatttttagaaaaagcgctgagtttaaagt 1047
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DB 23160 TAAATAATATTTATATATAAATATATTTTATTTAATATATATAAATATATATTTTATATT 23219

QY 1048 tatgaaaaa--gattgggtgactattccaattcaattagttgtgaaatgtagacaaatatttc 1105
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DB 23220 TAAATATATTTAATATATTTAATATATATTTATTTAATATATATTTATTTATATAAACAATATA 23279

QY 1106 atgagcaacaacaatcacagagaaataccaccctcgacgactacaacaactcctaagttaact 1165
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QY 1166 taatgaagcattgtagtaagggagctcagaataaaatttcttaaaatatttagaggaaaaact 1225
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DB 23340 AACATATATTTTATATTTAATATATATTTTATTTAATATATTTATATAAACAATATATTTT 23399

QY 1226 atttttaaaaaat-----tacaagaaaaagtttgatcctataaacctctttaaactttaaat 1280
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QY 1281 atctacaactttctctatgactcacatctggtgttgatgggtgattttgtcaaaatatatg 1340
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DB 23580 TTT--ATATTTAATATATATTTAATATTTAATATATATTTATTTAATATATACATATA 23637

QY 1461 laagcaacaataaataaaacattatacaagagatcaagataaatttaactatctatgaat 1520
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QY 1521 gtagaataatttttattataaatttgaaacta-aaattatcaaaataattcacaagtaaa 1579
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QY 1580 taatagatataaattcattccaataacgagtaaatccaactctattataatcatatattaga 1639
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QY 1760 gtagatgttaa---atgtaacgggttagactgagttttttgtattattattataaaa 1816
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QY 1817 tccattagagatttaagttaagtctctctcttgatttgaactggttctcaaaaattaggt 1876
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QY 1937 aatggttttttattcttgagagattgctcttagagattgaaattatgcttttgata 1986
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RESULT	4
DMU11584/c	
LOCUS	Drosophila melanogaster Oregon-R mitochondrial A+T region.
DEFINITION	4601 bp DNA linear INV 23-JUL-1994
ACCESSION	U11584
VERSION	U11584.1 GI:508826
KEYWORDS	mitochondrial DNA; A+T region; tandem repeats.
SOURCE	fruit fly.
ORGANISM	Mitochondrion Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 4601) Lewis,D.L., Farr,C.L., Farquhar,A.L. and Kaguni,L.S. Sequence, Organization and Evolution of the A+T Region of Drosophila melanogaster Mitochondrial DNA Mol. Biol. Evol. 11, 523-538 (1994)
REFERENCE	94285822
MEDLINE	
REFERENCE	2 (bases 1 to 4601) Kaguni,L.S. Direct Submission
AUTHORS	
TITLE	Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D, Dept. of Biochemistry, Michigan State University, East Lansing, MI, 48824-1318, USA
JOURNAL	
FEATURES	Location/Qualifiers 1..4601 /organism="Drosophila melanogaster" /organelle="mitochondrion" /strain="Oregon-R" /db_xref="taxon:7227" /dev_stage="embryo" 650..1022 /note="repeat I-A" /rpt_type=tandem 1023..1360 /note="repeat I-B1" /rpt_type=tandem 1361..1705 /note="repeat I-C/A" /rpt_type=tandem 1706..2043 /note="repeat I-B2" /rpt_type=tandem 2044..2388 /note="repeat I-C" /rpt_type=tandem 2491..2511 /note="deoxythymidylate stretch" 2512..2648 /partial /rpt_type=tandem 2649..3112 /note="repeat II-A" /rpt_type=tandem 3113..3576 /note="repeat II-B1" /rpt_type=tandem 3577..4040 /note="repeat II-B2" /rpt_type=tandem 4041..4504 /note="repeat II-C" /rpt_type=tandem complement(4565..4585) /note="deoxythymidylate stretch"
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repeat_unit	2271 a 131 c 74 g 2125 t
BASE COUNT	
ORIGIN	
Query Match	5.88; Score 143.6; DB 3; Length 4601;
Best Local Similarity	45.7%; Pred. No. 4.8e-10;
Matches 662; Conservative	0; Mismatches 774; Indels 14; Gaps 4;

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Qy	725	tatgattaaagtcgtatatatcggtgacaattgaagtttttccctcaagtttagccatttttat	784
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Qy	785	gaaattaaacttaactactactattaggcaaatcatcatctatcatcaacaattcaatg	844
Db	3435	ATTATTTATATAAATTAATAATAA--TAAATAAATATGACAATATATAAATTTTATATAA	3378
Qy	845	tgadtcaattttaccocaagattgaaagttgtgtgcaacttcgttcaactaaagttgta	904
Db	3377	TTATATCTACATTTTAAAAATTTTAAAAATTTTATTAATAATTTAGATATATAATAATA	3318
Qy	905	ttataaggttgacgactttaacctaaactattttgaaattgaaaggggttgatgacttcag	964
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Qy	965	ctttcaaaataattcaactaaagtcctgagactcacattggagatttttagtggttcacaaaatt	1024
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Qy	1025	ttagaataagggctgagttcaagtttgaaaaagattggtgactattccaattcaattagttg	1084
Db	3197	ATATTTTCATTTATAAAATTTATTTTAAAAAATTTTCTTTATTTTAAAAAACAATGAT	3138
Qy	1085	tgaattgatcaacaatatcttcgatgcataaccaatcagagaataccaacctgcagcacg	1144
Db	3137	TTTATTTATAATAATTTTTTTTAAAAAATTAATACATTTTAAGAAAT----TTTAAAAA	3083
Qy	1145	tacacaactccaatggttaattaaatgaagcattgagtaagaagctcagaatacaaat	1204
Db	3082	TTTATATTAATTTATTAATAATTTTAAATTTTCTATATATATATATATATATATTAAT	3023
Qy	1205	cttaaatattagaggaaaaactattttaaaaaattacaagaaaaagttgactataacct	1264
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Query Match 5.8%; Score 143.6; DB 3; Length 4601;
Best Local Similarity 45.7%; Pred. No. 4.8e-10;
Matches 662; Conservative 0; Mismatches 774; Indels 14;

[illegible]

D	b	11116	TATATAAATAATTTTATATAAATAATATATATTTTATATAAATAATATATAT-TTTTATATAAT	11174
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D	b	11175	ATAATTTTATATAAATAATATATTTTATATAAATAATATATTATATAAATAATATATTTTA	11234
Q	y	1831	aagttaaagtctctcttgattttaacaacagtggtctaaaaaatagggttcaat-cattgcgt	1889
D	b	11235	TATATAATATATATTTTATATAAATAATGTTATATATAATATAATATATATATATAATAT	11294
Q	y	1890	cctcaatgaacccactcatgtttttaaagtttttttgttttttgacaagtgttttttatt	1949
D	b	11295	ATATATTTTATATATACATATATTTTATATAAATAATATATATATATATATTTTATATAATA	11354
Q	y	1950	tctgagattgctccttaggattgaatttatgtttgatactagaacgaagaagtagagag	2009
D	b	11355	TATATATTTTATATAATATATATATATATATTTTGTAATAATATATATATATATATTTTA	11414
Q	y	2010	tagtgtatacacgctgtaaaaaataatagttgt	2041
D	b	11415	CATRAAAATATATATATTTTACATAATAATATAT	11446
R	E	S		
P	F	MALIP3/c		
L	O	CUS		
D	E	F	I	N
A	C	C	E	S
V	E	R	S	I
O	N			
O	R	G	A	N
R	E	F	E	R
A	U	T	H	R
T	I	T	L	E
J	O			
C	O	M	E	N
O	n	Dec 16,	1999	this sequence version replaced gi:5763807.
F	O	r more information about this sequence or the Malaria Project,		see http://www.sanger.ac.uk/projects/P.falciparum. IMPORTANT: This
s	e	quence is unfinished and does not necessarily represent the		correct sequence. Work on the sequence is in progress and the
r	e	lease of this data is based on the understanding that the		sequence may change as work continues. The sequence may be
p	h	age etc.		contaminated with foreign sequence from E.coli, yeast, vector,
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scores: Opt: 316, E(): 1.1e-12, (33.2% identity in 271 aa				
overlap)"				
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23896. .31533

rRNA

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PFB0110W, O96126 predicted integral membrane protein (255
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in 191 aa overlap)"
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/db_xref="GI:6594248"
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36744. .36749
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identity in 678 aa overlap"
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/gene="garp"

[illegible]

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3 6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-314B1, 2000 bp overlap; the clone sequenced to the right is RP11-86017. Actual start of this clone is at base position 161288 of RP11-314B1; actual end is at base position 168698 of RP11-813K12.

Data from AC069383 was used to finish this clone, AC068138. An unresolved di-trinucleotide repeat exists between 52436 and 52756.

FEATURES

source

Location/Qualifiers

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984. 1004

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1502. 1591

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1689. 1746

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5819. 5932

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6940. 7021

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Qy	1620	tattataatcatatcagatacaaatatacaaatatttggttaaaatttcacattatataatt	1679
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Qy	1680	actaaatatatttaattcttttgaatatctttttacacaagtaggtagacagagaagaatt	1739
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Qy	2031	ataatagttgt 2041	
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DEFINITION	Sequence 6 from Patent WO0200932.		
ACCESSION	AX344555		
VERSION	AX344555.1	GI:18492441	
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequence.		
REFERENCE	1 (sites)		
AUTHORS	Olek A., Piepenbrock, C. and Berlin, X.		
TITLE	Diagnosis of known genetic parameters within the mh		
JOURNAL	Patent: WO 020932-A 6 03-JAN-2002;		
FEATURES	Epigenomics AG (DE)		
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QY 724 gtaaggattaagtcgatatcggtgacaattggaatttctcctcaagtttagccatttta 783
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DB 8215 ATTAATAATAGTTTATTAATAAATAATAATAATTAATTTAAATAATATATAATAATAT 8156

QY 844 gtgagttcaatttaccagaagattgaaagttgtgtgcaactctgttaactaaagtgtg 903
DB 8155 TTAATAATAAATAA-----TTAATAATAATAATAATTTATTTATTTTCAATAATAA 8104

QY 904 attataaggttgacgactttaaccttaacttatttgaattgaggggttgacttca 963
DB 8103 AAATAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8044

QY 964 gctttaaaaaataactaactaaagttcttagactacattgagagatttttagtttcaaaaaa 1023
DB 8043 ATTATATTATTTTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 7984

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RESULT 13
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 ***, 3 unordered pieces.
 AC005504
 AC005504.3 GI:4558584
 VERSION

AC005504
 Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS
 ***, 3 unordered pieces.
 AC005504
 AC005504.3 GI:4558584

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	Unpublished 2 (bases 1 to 104992) Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W. Direct Submission Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT	On Apr 2, 1999 this sequence version replaced gi:4337172. * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
FEATURES source	* 1 58642: contig of 58642 bp in length * 58643 58842: gap of unknown length * 58843 91011: contig of 32169 bp in length * 91012 91211: gap of unknown length * 91212 104992: contig of 13781 bp in length. Location/Qualifiers 1..104992 /organism="Plasmodium falciparum" /db_xref="taxon:5833" /chromosome="12"
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Qy 731	ttaagtcgatcggtgcacaaattgaagtllcctaagaatttagccattttatgaatt 790
Db 73286	ATTAATATATATAATAAATAAATAATATAATAAATAAATAAATAAATAAAT 73345
Qy 791	aaacttaactactactaggtaaatcatatgatcataacaatttcaatgtgaatt 850
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Search completed: August 21, 2002, 02:28:10
Job time: 11106 sec

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Result No.	Query	Score	Match	Length	DB	ID	Description
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2	791.2	41.1	1864	18	AAAT73501	Poplar 1-aminocycl	
3	735	38.2	1888	18	AAAT73482	Papaya ACC synthas	
4	691.6	36.0	1868	18	AAAT73502	Poplar 1-aminocycl	
5	686.4	35.7	1878	19	AAV30326	Petargonium 1-amin	
6	672.8	35.0	2088	19	AAV20947	Coffee-fruit speci	
7	635.2	33.0	1113	18	AAAT72632	Mangifera indica A	
8	630.2	32.8	1775	12	AAQ15134	Clone ptACC1 encod	
9	630.2	32.8	1818	22	AAAD04546	Tomato 1-aminocycl	

DR WPI; 2000-270821/23.

DR P-PSDB; AAY79292.

XX Isolated nucleic acid molecule for producing transgenic plants having
PT altered characteristics such as resistance to a plant pathogen
PT comprises promoter, inducible in response to physical stimulation -
XX
XX
XX Claim 41; Page 98-101; 111pp; English.

CC The present sequence is that of cDNA encoding mung bean
CC 1-aminocyclopropane-1-carboxylic acid synthase (ACC synthase,
CC see AAY79292). The ACC synthase gene, AIM-1, is induced in response
CC to mechanical strain, auxin and salt stress. The invention
CC relates to the pCEL-1 promoter (see A294266) that directs
CC expression of the AIM-1 gene. pCEL-1 is capable of induction by
CC physical and/or environmental stimuli in cells in which it is
CC indigenous and, in the absence of any negative regulatory mechanism,
CC is capable of constitutive expression in cells in which it is
CC non-indigenous. The promoter can be used to direct expression of
CC genes conferring useful traits on plants, such as improved
CC resistance to a plant pathogen, altered nutritional characteristics,
CC expression of a plantabody, altered biochemical pathway, altered
CC fertility, and/or altered flower colour.

XX
SQ Sequence 1923 BP; 548 A; 383 C; 426 G; 566 T; 0 other;

Query Match 100.08; Score 1923; DB 21; Length 1923;

Best Local Similarity 100.08; Pred. No. 0;

Matches 1923; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	actccacactctaacacatacacacataatgggtttcaaggccatggacccaactcccttg	120
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Qy	121	ttgtccaagatggctattggggatggacatggcgaataatccccaatactttgatggtg	180
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Db	181	aaggcttatgatcaaaacccctttcatccacagataatcctaaacggtgttatgcaaatg	240
Qy	241	ggcttctgctggaatcagcttacctctctgatttgggtgaagattggatactgaacaacct	300
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Qy	301	gaagctccatttgcactccagaaggaataatgatatttcaggggccatagctaaactttcag	360
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Qy	361	gattatcatgtctggccgagttcagaataatgcttggctaaatttatggctagacaagg	420
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Qy	541	tattatccaggctttgacccggatttgggtggagaaacaggagtttaaacttgttccagtt	600
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Qy	601	atgtgcgtagctcaaaataattcgtttgacaagaaggaagcatttggagatgcctatgag	660
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Qy	661	aaagcaagagagataacatcagagttaaaggggtttactgatcaccaatccatcaaatcca	720
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Qy	721	ttaggcacaaatcatggacagaagaagacactgagaacogtggtagcttcatcaatgagaag	780
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Qy	781	cgtatccaccttgtagtgaataatatctgcaacagttttcagccaaacccgggttc	840
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Qy	841	ataagcatagctgagatattagagatgaacacagacatagagtgcaccgaacctcgta	900
Db	841	ataagcatagctgagatattagagatgaacacagacatagagtgcaccgaacctcgta	900
Qy	901	caactgtttatagctctttccaagacatgggttccctggcttcagagtcggcatcata	960
Db	901	caactgtttatagctctttccaagacatgggttccctggcttcagagtcggcatcata	960
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Db	961	tactcttacaatgatgctgtggttaattgtgcacgcaaaatgcgaagctttgattggtg	1020
Qy	1021	tcacacagactcagtatcttttagcatcgatgctaaatgatgatgatttctggagagg	1080
Db	1021	tcacacagactcagtatcttttagcatcgatgctaaatgatgatgatttctggagagg	1080
Qy	1081	ttcttggcagagagtgcaagagggttgcgtcaaaagtttcagggttttcaactgggggttg	1140
Db	1081	ttcttggcagagagtgcaagagggttgcgtcaaaagtttcagggttttcaactgggggttg	1140
Qy	1141	gccaaagttggcataaagtcgttgcacgcaaaatgcgtctatttctgttggatgattta	1200
Db	1141	gccaaagttggcataaagtcgttgcacgcaaaatgcgtctatttctgttggatgattta	1200
Qy	1201	aggaacttctcaaaaagccaaacttcgactctgaaacggagcttggaaagtatcatt	1260
Db	1201	aggaacttctcaaaaagccaaacttcgactctgaaacggagcttggaaagtatcatt	1260
Qy	1261	catgaagttagatcaaatgtttcacctggctattcttcctccactgcactgagcagggtg	1320
Db	1261	catgaagttagatcaaatgtttcacctggctattcttcctccactgcactgagcagggtg	1320
Qy	1321	tttaggggtgctatgccaacatggatgatatggctgtgcacaaatgctttgcacgaatc	1380
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Qy	1381	cgaacttctgcttccaaacaaagaggtcggtggtggttaataagaacaattgttggcac	1440
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Db	1561	atcgttttagaagaagtaactgatatgtgaagataacttgggttcttttatttattttg	1620
Qy	1621	agaaggtacataaagtgcgtggatttcttcttcttcttcttcttcttcttcttcttctt	1680
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Qy	1681	ttgttttgcgtagcgcacaaatccagtgctctacaagttgtgctgttcttcatgcacgc	1740
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 Db 1362 aaactagcttagactcagcttctctctctgctatgaggatcatcattgagacacccgggt 1421
 QY 1484 tcaccatgcaactcactctccctcactcagtcactcagtcactatggtttaagcca 1534
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RESULT 4

AAT73502
 ID AAT73502 standard; cDNA to mRNA; 1868 BP.
 XX
 AC AAT73502;
 XX
 DT 26-AUG-1997 (first entry)
 XX
 DE Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS2.
 XX
 KW Ozone; induction; exposure; resistance; transgenic plant; ACC;
 KW 1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.
 XX
 OS Poplar nigra.
 XX
 FH Key Location/Qualifiers
 FT CDS 119..1579
 FT /*tag= a
 FT /product= PNACCS2
 XX
 PN JP09075088-A.
 XX
 PD 25-MAR-1997.
 XX
 PF 07-SEP-1995; 95JP-0254510.
 XX
 PR 07-SEP-1995; 95JP-0254510.
 XX
 PA (TOYT) TOYOTA JIDOSHA KK.
 XX
 DR WPI; 1997-239270/22.
 DR P-PSDB; AAW21755.
 XX
 PT Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
 PT enzyme genes - from poplar tree, are useful for generating
 PT ozone-resistant trees and pollution clean-up trees

PS Claim 2; Pages 9-11; 12pp; Japanese.

CC This sequence, designated PNACCS2, is a 1-aminocyclopropane-1-
 CC carboxylic acid (ACC) synthase gene isolated from poplar trees which
 CC had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
 CC for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
 CC humidity, 30 k lux and air current 30 cm/second. This gene will be
 CC useful for breeding air pollutant ozone-resistant trees, especially
 CC poplar.

SQ Sequence 1868 BP; 590 A; 366 C; 405 G; 507 T; 0 other;

Query Match 36.0%; Score 691.6; DB 18; Length 1868;
 Best Local Similarity 71.7%; Pred. No. 2.8e-189;
 Matches 923; Conservative 0; Mismatches 359; Indels 6; Gaps 1;

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 QY 179 ggaaggttatgatcaaaacccctttcatccacagataatcctaacgggtgttatgcaa 238
 Db 198 ggaagcttacgataaaaaacccctttcacctactgacaaccccgatggagtaatacaa 257
 QY 239 tgggtcttgtagaatacacttactctctgatttgggtgaagattgtagatactgaacacc 298
 Db 258 tgggtctagcagaataacagcttccgctgattcgcattatagactggatcaagaacatc 317
 QY 299 ctgaagctccatttgcactccagaagaataaatatttcagggccatagctaaccttc 358
 Db 318 ccaagcctccatttgcactccagaagaataaatatttcagggccatagctaaccttc 377
 QY 359 aggtattatcatgtctgcccagagttcagaataatcgttggctaaatttatggctagaacaa 418
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 Db 438 gaggaggaaggtgacatttgatccagatcgcatagtcagcgggtggagcaactggag 497
 QY 479 cacagaagtcaactgcttttggcagatcccgccgagcaggtatttgcaggtcccttc 538
 Db 498 caaacgagctgacatgtttgctgcccagatcccgccgaggttcttctgtctctc 557
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QY 1319 ggttagggtgctatgccaacatgatgatgctgtgcaaatgctttgcaacgaa 1378
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QY 1379 tcgcgaactttgtcttcacaacaagga 1406
Db 1392 tacacgattgtcgttgacaacaagga 1419

RESULT 5
AAV30326
ID AAV30326 standard; cDNA; 1878 BP.
XX
AC AAV30326;
XX
DT 28-SEP-1998 (first entry)
XX
DE Pelargonium 1-aminocyclopropane-1-carboxylase synthase cDNA.
XX
KW ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
KW ethylene; transgenic plant; wilting; geranium; pPHSacc49; ss.
XX
OS Pelargonium x hortorum cv. Sincerity.
XX
FH Key
FT CDS 104..1576
FT /tag= a
FT polyA_signal 1810..1815
FT /tag= b
FT misc_feature complement (1..50)
FT /tag= c
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FT complement (301..350)
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FT complement (451..500)
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FT /note= "antisense oligonucleotide (Claim 13)"
FT complement (1..1878)
FT /tag= m
FT /note= "any contiguous 50 nucleotides (Claim 13)"
PN WO9814465-A1.
XX
PD 09-APR-1998.
XX
PF 30-SEP-1997; 97WO-US17644.
XX
PR 01-OCT-1996; 96US-0724194.
XX
PA (COLS ) UNIV COLORADO STATE RES FOUND.
XX
PI Ranu RS;
XX
PI WPI; 1998-260994/23.
XX
DR P-PSDB; AAW60235.
XX
PT New isolated ACC synthase genes - are obtained from geranium and
PT rose, used to develop products for producing plants with reduced
PT ethylene levels, for increasing shelf-life
XX
PS Claim 1; Fig 5; 77pp; English.
XX
CC This cDNA clone, designated pPHSacc49 (ATCC 98179), codes for a
CC 55.1 kDa 1-aminocyclopropane-1-carboxylate synthase (ACC synthase)
CC (see AAW60235) of geranium (Pelargonium x hortorum cv. Sincerity).
CC High quality mRNA was obtained from flower tissue using a novel
CC adaptation of the 2-butoxyethanol precipitation technique. This
CC was converted to cDNA and screened with a probe generated by PCR
CC amplification (see AAV30328-29). The pPHSacc49 clone was obtained.
CC Geranium ACC synthase cDNA clones pHSacc41 (see AAV30324) and
CC pPHSacc44 (see AAV30325), and rose ACC synthase cDNA clone pRoseKacc7
CC (see AAV30330), are also claimed. These ACC synthase genes, or their
CC fragments, when introduced in antisense orientation under control
CC of a strong promoter, can be used to genetically modify a plant,
CC especially geranium, rose or woody plant. As a consequence, the
CC amount of ACC synthase produced in the plant cells is reduced and
CC the rate of ACC conversion to ethylene decreases. This can be used
CC to prolong the shelf-life of cut flowers and to reduce leaf
CC yellowing and petal abscission during shipping and storage.
XX
SQ Sequence 1878 BP; 569 A; 390 C; 432 G; 487 T; 0 other;

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Query Match 35.7%; Score 686.4; DB 19; Length 1878;
Best Local Similarity 70.8%; Pred. No. 9e-188;
Matches 1001; Conservative 0; Mismatches 396; Indels 17; Gaps 6;

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Db 189 actttgatggctggaaagcttacgacaacaatcccttccatcccaaaacccctcaag 248
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RESULT 6
AAV20947
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XX
AC AAV20947;
XX DT 07-JUL-1998 (first entry)
XX DE Coffee-fruit specific ACC synthase cDNA.
XX KW Coffee-fruit; 1-aminocyclopropane-1-carboxylic acid synthase;
XX KW ACC synthase; ethylene biosynthesis; fruit ripening; ss.
XX OS Coffea arabica.
XX FH Key
XX FT CDS 187..1701
XX FT /*tag= a
XX FT /product= ACC_synthase
XX PN WO9806852-A1.
XX XX 19-FEB-1998.
XX PF 11-AUG-1997; 97WO-US14184.
XX PR 12-AUG-1996; 96US-0695412.
XX PA (UYHA-) UNIV HAWAII.
XX PI Moisyadi I, Neupane KR, Stiles JI;
XX WP 1998-159543/14.
XX DR P-PSDB; AAW52818.
XX PT ACC synthase and ACC oxidase from coffee, Coffea arabica - and
XX PT encoding DNA, useful in methods to control coffee bean ripening e.g.
XX PT to allow synchronous ripening and thus more productive harvesting
XX PS Claim 2: Fig 2; 72pp; English.
XX CC The present sequence encodes Coffea arabica, coffee-fruit specific
XX CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase.
XX CC ACC synthase cDNA can be used to control ethylene biosynthesis in
XX CC coffee plants, as ACC synthase is an element of the ethylene
XX CC biosynthesis pathway. Transformation of wild-type coffee plants
XX CC with constructs containing the cDNA in an antisense orientation
XX CC can block ACC synthase synthesis. The cDNA can also be used to
XX CC block ACC synthase synthesis by co-suppression. Plants transformed
XX CC with the cDNA are incapable of synthesising ethylene, which is
XX CC necessary in the final stages of fruit ripening in coffee,
XX CC therefore ethylene application enables fruit ripening to be
XX CC controlled, e.g. application to the entire plant can synchronise
XX CC ripening. Coffee beans are preferably obtained from mature fruit,
XX CC but non-uniform ripening has necessitated laborious hand-picking,
XX CC or low yields and productivity when harvesting by strip harvesting
XX CC or mechanical techniques. The ability to synchronise ripening
XX CC makes mechanical harvesting more productive.
XX SQ Sequence 2088 BP; 599 A; 421 C; 432 G; 636 T; 0 other;

Query Match		35.0%	Score 672.8	DB 19	Length 2088
Best Local Similarity		70.7%	Pred. No. 8.1e-184		
Matches	912	Conservative	0	Mismatches 372	Indels 6
Qy	106	gaccaaacctcccttgctgcagagatggctctattggggatggacatggcgaaatcatcccca	161		
Db	208	gaccaaacacaaactctgtcgaagatggcaaccaacgatggacatggcgaaaaactcgctt	267		
Qy	166	tactttgatgatggaaaggtcttatgatcaaaacccctttcatccacacagataaactcaac	225		
Db	268	tattttgatggttggaaagcatatgatgatctctaccatccaccagaaatctccta	327		
Qy	226	ggttttatgaaatgggtcttctgtagaatcagcttaactctgatttggttggaagattgg	288		
Db	328	ggttttatcagatgggaactcgcagaataatcagttatgctttgatttgatcgaggaatg	387		
Qy	286	atactgaacaacctgaagccctccatttgcactccacagaaggaataaattgatttcaggcc	345		
Db	388	gttcgaaacaatccagaggtctccatttgcacagcagaaggagcgacaaattcatgaa	447		
Qy	346	atagtaactttcagatattcatggtctggccaggttcagaaatgcgtggctaaattt	405		
Db	448	gttgctatctatcaagatlatcatggttcgcaagattcagaataatgctgtgagcaagttc	507		
Qy	406	atggctagaacaaggggaaacagatacgtctttgacctgacctgattgtcatgagcgtt	465		
Db	508	atggagaaggtgagaggtgacagatcgaattcgatcccaacgcattgtgatgagtgtt	567		
Qy	466	ggagccaccggagcacaggaagtcaactcttttggttggcagatcccgcgaggcattc	525		
Db	568	ggggcaacccggagctatgaactctgggctctgtttagctgacctgaagatgcgttt	627		
Qy	526	ttagtgccattccctattatccagcttttgaccgggatttgaggctggagacagagatt	585		
Db	628	ttgtgtaccacacattatccagatttgatcgggatttgagggtggcgacagggatg	687		
Qy	586	aaatttgttccagttatgtgcgatagctcaataaattctgcttgacaaaggaaagcattg	645		
Db	688	caactcttccaaattgttctgcagctccaaatgattttaagctcaataagaatccatg	747		
Qy	646	gaagatgcctatgagaagaacagagagataaacatcagatgaagggtttactgatccc	705		
Db	748	gaagctgcttatcagaagctcaagaagcacaatcagatgaaggggttctcttaaat	807		
Qy	706	aatcatcaaatccattagggcacatcatggacagaaagacacactgagaacggctgtagc	765		
Db	808	aatcatcaaatccatttggaaactgttctgcaggaaacittgatgatataatccaca	867		
Qy	766	ttcataatgagagcgtatccacctgtatgtgatgaataatatgctgcacagttttc	825		
Db	868	ttcataatgacaaaaataccaccttgattgttgatgagatatacttgcacacgtcttc	927		
Qy	826	agccaacccggattcataagcatagctgagatattagagatgaacacagacatagatgt	885		
Db	928	agccagccgaattcatcagcatctctgaaataattggagcat-----gatgttcaatgc	981		
Qy	886	gaccgcaacctctgtacacattgtttatagctcttccaaaggacatgggttccctggctt	945		
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Qy	946	agagtgcgcacataactcttacaatgatgctgtgtggttaatttgcacgcgaaaatgtca	1005		
Db	1042	agaattggcaatttgtatcaataatgacgtgtgttgcagcttgcgtagaaaaatgtcg	1101		
Qy	1006	agctttggatttggctcaacacagactcagtatcttttagcatcgatgctcaaatgatgt	1065		
Db	1102	agtttgggcttcttcaacacaaactcagcatctcga ttcgatcaatgttcatcggacga	1161		
Qy	1066	gagtttggagagggttcttggcagagagtgcgaaggttggctcacaaggttccagggtt	1125		
Db	1162	gcatttatggacaaaatcatcttccacgagctcagagagattagctgcagagccatgtctt	1221		
Qy	1126	ttcaactggggggttggccaaagtggcataaagtcttgcgaagcaatgctgtgctattt	1185		

Db	1222	ttcacaaggagcattgctcaagtaggcattggcaccttaaaagcagtgcggcctttat	1281
QY	1186	gtgtggatggatttaaggcaactctcaaaaagcgaactttgcactctgaaacggagcctt	1245
Db	1282	ttctggatggacttaaggagactcctcagggaagtcacatttgaggcagaatacggaactt	1341
QY	1246	tggaaagtttatcatctatgaatttaagatacaattttccactggcctattccttccattgc	1305
Db	1342	tggaggatcataatacatgaagtcgaagtcgaattttccaccaggcttatctttccattgc	1401
QY	1306	actgagccagggtggttttagggctgctatgcacaactggatgatatggctgtgcaaat	1365
Db	1402	tcagaaaccaggagcttcagagtgtgctttgccaactggacgacgaagtgtgagagtt	1461
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Db	1462	gtctccagaagaataccacaaatttgtgctt	1491

RESULT	7	
AAT72632		
ID	AAT72632	standard; DNA; 1113 BP.
XX		
XX	AAT72632;	
XX		
XX	27-JAN-1998	(first entry)
DT		
XX	Mangifera Indica	ACC synthase mlacc2 gene.
DE		
XX		
KW	ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase	
KW	mlacc2; ethylene biosynthesis; transgenic plant; senescence;	
KW	antisense expression system; plant development; fruit ripening;	
KW	EC 4.4.1.14; mango; multigene family; ss.	
XX		
OS	Mangifera indica.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	1..1113
FT		/tag= a
FT		/EC.number= 4.4.1.14
FT		/product= mlacc2
FT		/note= "Sequence represents 75% of the coding
FT		sequence and does not contain the start
FT		or stop codons."
FT		

WO711166-A1.
 27-MAR-1997.
 20-SEP-1996; 96WO-AU00591.
 02-MAY-1996; 96AU-0009603.
 20-SEP-1995; 95AU-0005559.
 (UYQU) UNIV QUEENSLAND.
 Botella JR;
 WPI, 1997-202875/18.
 P-PSDB; AAW18290.
 Pineapple, papaya and mango ACC synthase genes - used in gene therapy to produce fruits with reduced senescence
 Claim 5; Fig 5; 46pp; English.

This sequence represents the novel gene, *miacc2*, which is a member of the mango ACC synthase multigene family. ACC synthase an enzyme involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical

CC wounding has occurred and diminishes their post harvest quality and
CC storage life. Novel ACC synthase genes expressed in transgenic plants
CC using either sense or antisense expression system may be used to control
CC the regulation of plant development, in particular fruit ripening,
CC reducing senescence and thus improving storage life.
XX
SQ Sequence 1113 BP; 320 A; 212 C; 264 G; 317 T; 0 other;

Query Match 33.0%; Score 635.2; DB 18; Length 1113;
Best Local Similarity 74.3%; Pred. NO. 4.e-173;
Matches 831; Conservative 0; Mismatches 278; Indels 9; Gaps 2;
QY 235 caaatgggtcttgctgagaatacagcttaccctctgtgttggttgaagattgatactgaac 294
DB 1 cagatgggatttggggaaatctgtctgttctgtttagttcagaagaatgggtcttaagc 60
QY 295 aacctgaagctccattgactccagaagaataaaatgatttcaggggccatagctaac 354
DB 61 aaccagaagctctatctgactccgaaggtataagtgatttcagagatactctatc 120
QY 355 ttccaggattatcatgtgtgtccgagttcagaataatgctgtgtgctaaattttatggctaga 414
DB 121 ttccaggattatcacggcttgcagagttcagaataatgctgtgtgcaaatttttatggcaaga 180
QY 415 acaagggaacacagatcacgtttaccctgacgttattgttcattgagcgggtgagccacc 474
DB 181 gtgaggggaatagatgataacacacctgacgtatgtaattgttatgagcgggtgagcaacc 240
QY 475 ggagcacacgaagtacgtcttctgttggcagatcccgcgagggcattcttagtgccc 534
DB 241 ggagcacatgagacgttgccttctgttggcgtgctacccgggtgaagcatttttgggtgcc 300
QY 535 attccctattatccaggctttgaccgggattgaggtggagaaacagggagttaaactgtt 594
DB 301 actccttactccaggattgtgtcgagattgagattgagagagagaggttcaactttt 360
QY 595 ccagttatgtcgatagctcaataattctgtgttgacaaaggaaagacattggaagatgcc 654
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QY 655 tatgagaagcaagagagataacatcagagtaaagggtttactgatcaccaatccatca 714
DB 421 tatgaaaagctcaagagacacatcagaaatcaagggttggctcctcaacaatccatcg 480
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DB 481 aaccgcctgggagcttgttgacagagaaacactaagaagtttagtaagcttcaattaa 540
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QY 832 ccggttttcaataagcatagctagatattagaggtgaaacacagacatagagtgcacgc 891
DB 601 ccgatttcatgcatctctgaaattatagaaga-----agatatcactgcaatgcg 654
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DB 655 aatctcatccacctgttttacagttctttcaaggatctggggttcccgagctttagggtc 714
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DB 715 ggcattatatactacaacatgacagttgtgtgtgtgcgcctgcgaatgtcaagcttt 774
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QY 1192 atggatttaaggcaacttctcaaaagccaaactttcgaactctgaaacgagcgtttggaaa 1251
DB 955 atggatttgcatactctcctcaagagcaaaactgatgaagcagagataagaactgtggaaa 1014
QY 1252 gtatcatctcatgaagttaagatcaatgtttccactggcttattccttcattgcactgac 1311
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DB 1075 ccagatggttcgggttgttctccaaatggacga 1112
RESULT 8
AAQ15134
ID AAQ15134 standard; DNA; 1775 BP.
XX
AC AAQ15134;
XX
DT 17-DEC-2001 (updated)
DT 09-MAR-1992 (first entry)
XX
DE Clone pACC1 encoding the tomato ACC synthase.
XX
KW 1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening; ss.
XX
OS Lycopersicon esculentum c.v. Rutgers.
XX
FH Key Location/Qualifiers
FT CDS 91..1548
FT /*tag= a
FT polyA_signal 1732..1737
FT /*tag= b
XX
XX USN7579896-N.
XX
PD 12-NOV-1991.
XX
PF 10-SEP-1990; 90US-0579896.
XX
PR 10-SEP-1990; 90US-0579896.
XX
PA (USDA) US SEC OF AGRICULTURE.
XX
PI Theologis A, Sato T;
XX
DR WPI; 1991-368895/50.
DR P-PSDB; AARI5506.
XX
DNA encoding ACC synthase - used for control of plant development
and for prodn. of ACC synthase, ethylene and ethanol
XX
PS Disclosure; Fig 8; 73pp; English.
XX
CC A lambda gt10 library was constructed using cDNA prepared from polyA
RNA isolated from powdered, frozen fruit (i.e. tomatoes).
CC Recombinant phage containing inserts were plated, transferred to
CC a nitrocellulose filter and hybridised to zucchini pACC1 cDNA as
CC probe (see AAQ15131). A full-length cDNA from tomato, designated
CC pACC1 was recovered. Additional clones were isolated using the
CC 3'-end of pACC1 as a probe.
CC See also AAQ15132-Q15140.
CC (Note: Revised entry submitted to correct the patent number format of
CC US Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)
XX
SQ Sequence 1775 BP; 589 A; 279 C; 362 G; 545 T; 0 other;

Query Match 32.8%; Score 630.2; DB 12; Length 1775;
Best Local Similarity 65.4%; Pred. No. 1.5e-171;
Matches 961; Conservative 0; Mismatches 493; Indels 15; Gaps 2;

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DB 54 aattttcttcaactctaaactcatttagtaaaaaaaatggattgagattgcaaaagac 113
QY 111 aactcccttgggttcagagatggcttatgtgggatggagacatgacgcaatcccccatact 170
DB 114 caactcaactctatcaaaattggctactaaatgaagagatggcgcaaaactcgccatatt 173
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DB 174 tgatgggtggaagatcacgtagtgatcctttccaccctctataaaaccccaacggagt 233
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DB 1491 tgaaagtgtttgtcaccactttcgtcac 1519
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RESULT 9

AA04546
ID AAD04546 standard; cDNA; 1818 BP.

XX AC AAD04546;

XX DT 04-JUL-2001 (first entry)

XX DE Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2 cDNA.

XX KW Tomato; 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC2;
ethylene production; fruit ripening; transgenic plant; ss.

XX OS Lycopersicon esculentum.

XX FH Key Location/Qualifiers
XX CDS 91..1548

XX FT /*tag= a

XX FT /product= "Tomato LE-ACC2"

XX FT /transl_except= (pos:460..462, aa:Ala)

XX PN US6207881-B1.

XX PD 27-MAR-2001.

XX PF 25-JAN-1995; 95US-0378313.

XX PR 19-APR-1992; 92US-0862493.

XX PR 10-SEP-1990; 90US-0579896.

XX PA (USDA) US SEC OF AGRIC.

XX PI Theologis A, Sato T;

XX DR WPI; 2001-289591/30.

XX DR P-PSDB; AAE00984.

XX PT Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic
acid synthase, LE-ACC2 useful for producing ACC synthase which is
essential for the production of ethylene in higher plants

XX
PS
XX

Claim 1; Fig 5; 92pp; English.

The present sequence is a cDNA encoding tomato (Lycopersicon esculentum) 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2. ACC synthase are capable of catalysing the conversion of AdoMet (S-adenosyl methionine) to ACC and methyl thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which is essential for the production of ethylene in higher plants, where ethylene is a determinant of fruit ripening. The ACC DNA is also useful for producing transgenic plants which are overproducers of or are deficient in ACC synthase.

XX
SQ Sequence 1818 BP; 602 A; 282 C; 367 G; 567 T; 0 other;

Query Match 32.8%; Score 630.2; DB 22; Length 1818;

Best Local Similarity 65.4%; Pred. No. 1.6e-171;

Matches 961; Conservative 0; Mismatches 493; Indels 15; Gaps 2;

QY 51 acttttttacctccacactctaaacacatacacatataatggttttcaaggccatggacca 110
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QY 111 aactcccttgttccaagatgctattgggatggatgacatgacgaatcatcccatcatt 170
DB 114 caactcaattatcaaaattggtactaatgaagatgacgaataactgcacataatt 173
QY 171 tgatggatgaaagggttatgatcaaaacccctttccacacagataactcctaaccggtg 230
DB 174 tgatgggtgaaagcatagatagatgctttccacccctctaaaaaccccaacggagt 233
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DB 531 accttaccatactaccagcatttaacagagatttaagatggagacacaggagttacaact 590
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DB 591 tatccaattcactgtagagctcccaataatttcaaaattacttcaaaagcagtaaaaga 650
QY 651 tgctatgagaagaagaagagagataacatcacagataaagggttttactgatcccaatcc 710
DB 651 agcatatgaatgcaaaaaatacaaatcaaaagtaaaaggttgcattttgaccaatcc 710
QY 711 atcaaatccattagggacacaaatcatggacagaagaacactgagaaacggtggtgcttcat 770
DB 711 atcaaatccattagggacacaaatcatggacagaagaacactgagaaaggttgcattttcac 770
QY 771 caatgagaagcgtatccacttgatgataatataatgctgcaacagttttcagcca 830
DB 771 caaccaacaacaatccacttctgttgcagaaattctacgcagccactgtctttgacac 830
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DB 831 gctcaatttcgctcagtagctgaaatcctcgtgatgaacaggaaatgacttactgcaaca 890
QY 891 caacctcgtacacattgtttatatgttttcaaaaggacatgggttccctcgttcagagt 950
DB 891 agatttagttcacactcgtctacagtcttcaaaagacatgggttaccaggtattagagt 950
QY 951 cggcatcatactcttacaatgactgctggttaattgtgcacgcaaaatgccaagctt 1010
DB 951 cggaaatcatactcttcaaacgacgatgcgttaattgtctagaaaaatgctcagagtt 1010
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DB 1011 cggtttagtatctacacaaacgcaatatttttagcggcaatgctatcgcacaaaaatt 1070
QY 1071 tgtggagaggtttctgcagagagtgcaaaagaggttgcgtcctcaaggttcagggttttcc 1130
DB 1071 cgtcgataattttctaaagaaagcgcgtgaggttaggttaaaggcacaacattttac 1130
QY 1131 tggggggttggccaaagtggcataaagtcttgcaaaagcaatgcgtggtctatttgggt 1190
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DB 1251 agttattaaacgatgttaagcttaacgtctgcctggatctcgtttgaatgcaaga 1310
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DB 1371 cgcgagattcggaggttcgttagttgagaaaagtggagataaatcgatttcgatgga 1430
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DB 1431 aaagaagcaacatggaagaagaataattgagacttagtttttcgaaaagaatgatga 1490
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RESULT 10

AAV15704

ID AAV15704 standard; cDNA; 2230 BP.

XX AAV15704;

XX 01-JUN-1998 (first entry)

XX Tomato ACC synthase cDNA.

DE Tomato ACC synthase cDNA.

XX Tomato; ACC synthase; conserved peptide;

KW 1-aminocyclopropane-1-carboxylic acid synthase;

KW delayed fruit ripening; transgenic plant; ss.

XX Lycopersicon esculentum.

OS Lycopersicon esculentum.

XX Key Location/Qualifiers

FT CDS 91..1548

FT /tag= a

FT /product= ACC_synthase

XX US5723766-A.

PN 03-MAR-1998.

XX 07-JUN-1995; 95US-0481171.

XX	02-APR-1992;	92US-0862493.
PR	10-SEP-1990;	90US-0579896.
PR	25-JAN-1995;	95US-0378313.
PR	07-JUN-1995;	95US-0481171.
XX		
PA	(USDA) US SEC OF AGRIC.	
XX		
PI	Sato T, Theologis A;	
XX		
DR	WPI; 1998-206005/18.	
DR	P-PSDB; AAW47313.	
XX		
XX		
PT	DNA encoding anti-sense RNA blocking plant ACC synthase expression -	
PT	is used for producing transgenic plants with delayed fruit ripening	
XX		
PS	Example 3; Columns 63-68; 91pp; English.	
XX		
CC	The present sequence encodes tomato	
CC	1-aminocyclopropane-1-carboxylic acid (ACC) synthase. Tomato ACC	
CC	synthase was used in the isolation of conserved sequences from	
CC	five tomato (LB-ACC 1A, LE-ACC 1B, LE-ACC2, LE-ACC3 and LE-ACC4)	
CC	and two zucchini (CP-ACC 1A and CP-ACC 1B) ACC synthases.	
CC	A novel DNA molecule comprises an expression system which, when	
CC	contained in a plant host cell, generates RNA that is sufficiently	
CC	complementary to an RNA transcript of an endogenous ACC synthase	
CC	gene to prevent its synthesis. The expression system consists of	
CC	the reverse transcript of the antisense RNA (i.e. cDNA) operably	
CC	linked to control sequences that effect its transcription into the	
CC	antisense RNA, where the cDNA can be amplified from the endogenous	
CC	ACC synthase gene by primer pairs encoding conserved ACC synthase	
CC	sequences. The DNA molecule can be used to delay ripening of	
CC	tomato or zucchini fruits.	
XX		
SQ	Sequence 2230 BP; 824 A; 314 C; 414 G; 678 T; 0 other;	
Query Match		
Best Local Similarity 32.8%; Score 630.2; DB 19; Length 2230;		
Matches 961; Conservative 0; Mismatches 493; Indels 15; Gaps		
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Db	54	aatcttcactcttaaacactatttagtaaaaaaaatgggtatttgagattgcaaacac 113
QY	111	aactcccttgtgtccagatggcgtatttggggatggacatggcgaatcatcccatctt 170
Db	114	caactcaactctatcaaaaattggtactaatgaagcatggcgaaaactcgccatattt 173
QY	171	tgatgtatgggaaggtctatgatcaaaaccccttcatcccacagataaacttaacggtgt 230
Db	174	tgatgggtggaaagcatacagatgatctcttccaccctctctaaaaaccccaacggagt 233
QY	231	tatcgaatgggtcttctctgagatcagcttacctctgatattggttgaagattgatctact 290
Db	234	tatcgaatgggtcttctgtaaatcagcttgttttagcttgatagaagattgattaa 293
QY	291	gaacaacccctgaagcctccatttgcactccagaaggaataaatgattccagggccatagc 350
Db	294	gagaaccccaaaaggttcaatttg---tctgaagggaatcaaatcattcaagggccattgc 350
QY	351	taactttcaggaatatatgggtctggccaggttcagaaatgcttggtctaaatttatggc 410
Db	351	caactttcaagatttatcatgcttgcctgaattccagaaaagcagattgcgaatttatgga 410
QY	411	tagaacaagggaacacagaatacagttttgacctctgacctgacogtatttgtcatgagcgtt 470
Db	411	gaaaaacaagggaaggaaggttagatttgatccagaaagagttgttaagtgttggtgtgc 470
QY	471	cacggtgacacacgaagtcactgaccttttggttggcaatccccggcggagcattcttagt 530
Db	471	cactggagctaatgagacaattatatttggttggctgatcctggcgatgcatttttagt 530

RESULT 11
AAD04544
ID AAD04544 standard; DNA; 2230 BP.
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Qy	531	gccattccctattatccaggctttgaccggatttgaggtgagaaacaggagattaaact	590
Db	531	acctccactactaccagcatttaacagagatttaagatggagacctgggtacaaact	590
Qy	591	tgttccagttatgtgcgatgcataataatttcgtgttgacaaaaggaagcattggaga	650
Db	591	tattccaatcactgtgagagctccataatttccaaattacttcaaaagcagtaaaaga	650
Qy	651	tgcctatgagaagaagagagatacaacatccagagttaaaggttttactgatccaaatcc	710
Db	651	agcatatgaaaaatgcacaaaaatcaaacatcaagtaaaaggttgattttgaccaatcc	710
Qy	711	atcaaatccattaggcacaaatcatgacagagaagacactgaaacogtggtagattcaat	770
Db	711	atcaaatccattgggcaccactttggacaaaagacacactgaaagatgtcttgagttcac	770
Qy	771	caatgagaagcgtatccactgtatgtgatgaatatatgtctgcacagttttcagcca	830
Db	771	caaccaacaacatccactgtttgtgacgaatactacgcagcactgctcttgacac	830
Qy	831	aocgggtttcataagaatagctgagatatattagagatgaacacagacatagagtgacgg	890
Db	831	gcctcaattcgtcgtatagctgaaactcctcgtatgaacagaaaatgacttactcaacaa	890
Qy	891	caactcgtacacattgtttatagctcttccaaagacatgggttccctggcttcagaagt	950
Db	891	agatttagttcaactcgtctacagctcttccaaagacatgggttccctggcttcagaagt	950
Qy	951	cggcatcatactcttcaaatgatcgtgtgttaattgtgtcgcgcaaaatgtcaagctt	1010
Db	951	cggaaatcatattcttttaacgacga tgcgtcaattgtctagaaaaatgtcgagttt	1010
Qy	1011	tggatgtgtgtcaacacagactcagta tcttttagactcgtatcctaataatgatgatgatt	1070
Db	1011	cggtttagtatctcacaaaaacgcgaatttttttagcgggcaatgcta cggacaaaaaatt	1070
Qy	1071	tgtgagaggtttctgcgacagagtgcaaaagaggttgcttcaagggttcagggtttttcac	1130
Db	1071	cgtcgataattcttagagaaaagcgcgtagggttaggttaaaaggcacaacattttac	1130
Qy	1131	tgggggggttggccaaagtgtggcaaaaagccaaactctgcactcgaacggagaggtttggaa	1190
Db	1131	taa tggacttgaagtgtgggaattaaatgcttgaaaaaaa taa tgcggggcctttttgttg	1190
Qy	1191	gatgatttaaggcaactcttcaaaaagccaaactctgcactcgaacggagaggtttggaa	1250
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Db	1251	agttattataaacgagttaagcttaacgtctcgcgtgatcttcgtttgaaatgtcaaga	1310
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Db	1311	gccagggtgtgtccagttgttttgc aaatatggatga tggaaacgggttgatctgcgt	1370
Qy	1371	gcaacgaatccgcaacttgt -----gcttcaaaaacaggaggtcgtgtgttc	1418
b	1371	cgcgaggattcgggggtgtcgttaggtgttgagaaaagtgagataaaatcgaggttcgatgga	1430
Qy	1419	taataagaacaactgttggcacaagtaacttgaggtcgtacgtccataaaacagaaggttga	1478
b	1431	aaagaagcaacaatggaagaagaataatttgagacttggttttgcgaagaagaatgata	1490
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RESULT 11
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ID AAD04
XX


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Db 1134 cgtcgataattttctaagagaaagcgcgatgaggttaggttaaaagcacaacattttac 1193
Qy 1131 tggggggttgccaaagtggcataaagtgccttgcaagcaatgcgtgcttatttgtgtg 1190
Db 1194 taatggacttgaagttagtgggaattaaatgcttgaaaaataatgcggccttttgttg 1253
Qy 1191 gatgatttaaggcaacttctcaaaaagccaaactttcactctgaacgggagctttgaa 1250
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Qy 1251 agttatcatcatgaagttaagatacaatgtttcaccttgctattcctccattgcactga 1310
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Qy 1371 gcaacgaatccgcgaactttgt-----gcttcaaaacaaaggaggtcggtgtc 1418
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Db 1554 tgaaagtgtttgtcaccactttcgtcac 1582

RESULT 14
AAV30325
ID AAV30325 standard; cDNA; 2678 BP.
XX
AC AAV30325;
XX
DT 28-SEP-1998 (first entry)
XX
DE Pelargonium 1-aminocyclopropane-1-carboxylase synthase cDNA.
KW ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
KW ethylene; transgenic plant; wilting; geranium; pPHSacc44; ss.
XX
OS Pelargonium x hortorum cv. Sincerity.
XX
FH Key Location/Qualifiers
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FT /*tag= b
FT polyA_signal 2635..2640
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XX
PN WO9814465-A1.
XX
XX 09-APR-1998.
PD
PF 30-SEP-1997; 97WO-US17644.
XX
PR 01-OCT-1996; 96US-0724194.
XX
XX (COLS ) UNIV COLORADO STATE RES FOUND.
XX
PI Ranu RS;
XX
DR WPI; 1998-260994/23.
DR P-PSDB; AAW60234.
XX
PT New isolated ACC synthase genes - are obtained from geranium and
PT rose, used to develop products for producing plants with reduced
PT ethylene levels, for increasing shelf-life
XX
PS Claim 1; Fig 4; 77pp; English.
XX
CC This cDNA clone, designated pPHSacc44 (ATCC 98178), codes for a
CC 54.2 kDa 1-aminocyclopropane-1-carboxylate synthase (ACC synthase)
CC (see AAW60234) of geranium (Pelargonium x hortorum cv. Sincerity).
CC High quality mRNA was obtained from flower tissue using a novel
CC adaptation of the 2-butoxyethanol precipitation technique. This
CC was converted to cDNA and screened with a probe generated by PCR
CC amplification (see AAV30328-29). The pPHSacc44 clone was obtained.
CC Pelargonium ACC synthase cDNA clones pHSacc41 (see AAV30324) and
CC pPHSacc49 (see AAV30326), and rose ACC synthase cDNA clone prosekacc7
CC (see AAV30330), are also claimed. These ACC synthase genes, or their
CC fragments, when introduced in antisense orientation under control
CC of a strong promoter, can be used to genetically modify a plant.
CC especially geranium, rose or woody plant. As a consequence, the
CC amount of ACC synthase produced in the plant cells is reduced and
CC the rate of ACC conversion to ethylene decreases. This can be used
CC to prolong the shelf-life of cut flowers and to reduce leaf
CC yellowing and petal abscission during shipping and storage.
XX
SQ Sequence 2678 BP; 738 A; 550 C; 687 G; 703 T; 0 other;
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Query Match 32.6%; Score 627; DB 19; Length 2678;
Best Local Similarity 66.6%; Pred. No. 1.6e-170;
Matches 913; Conservative 0; Mismatches 455; Indels 3; Gaps 1;
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Db 64 tgtcaagattgcaaccaacgacgacacggcgagaactccccatttcgatggttga 123
Qy 182 aggccttatgatcaaaacccctttccaccacagataactcaacggtgtatgcaaatg 241
Db 124 aggccttatgacggtgatcgttccatccgttcacagataactcaacggtgtatccagatg 183
Qy 242 gctcttgagaatacagcttacctctgatgttgggtgaagatggactgaactgaacacctg 301
Db 184 gtttagctgaaaaatcagctttcatctgactgtatgataagatgggtgaggtccaacccag 243
Qy 302 aagcctccatttgcactccacgaaggaataaatgatttcaggggccatagctaatcttccagg 361
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OM nucleic - nucleic search, using sw model

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Searched: 383533 seqs, 122816752 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	673.8	35.0	2040	2	US-08-695-412B-11
4	635.2	33.0	1113	3	US-09-043-627-9
5	630.2	32.8	2230	4	US-08-378-313-24
6	627	32.6	1800	1	US-07-809-457A-8
7	627	32.6	1800	1	US-08-553-943-8
8	627	32.6	1800	5	PCN-US91-09437-8
9	627	32.6	2678	1	US-08-724-194-2
10	625.4	32.5	1945	1	US-08-724-194-1
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24	304.2	15.8	994	2	US-08-860-577-7
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28	249.4	13.0	1384	2	US-08-860-577-1	Sequence 1, Appl1
29	216.6	11.3	961	4	US-08-846-826A-3	Sequence 3, Appl1
30	70	3.6	159	2	US-08-463-418-3	Sequence 3, Appl1
c	44.4	2.3	7218	1	US-08-232-463-14	Sequence 14, Appl1
31	44.4	2.3	800	1	US-08-434-705B-7	Sequence 7, Appl1
32	39.2	2.0	800	2	US-09-086-201-7	Sequence 7, Appl1
33	39.2	2.0	2483	1	US-08-434-705B-9	Sequence 9, Appl1
34	39.2	2.0	2483	2	US-09-086-201-9	Sequence 9, Appl1
35	39.2	2.0	1701	3	US-08-599-968-2	Sequence 2, Appl1
36	37.6	2.0	5506	4	US-09-004-838-93	Sequence 93, Appl1
c	35.2	1.8	2444	3	US-08-906-791-1	Sequence 1, Appl1
37	34.8	1.8	2469	4	US-09-111-730-5	Sequence 5, Appl1
38	34.8	1.8	2558	4	US-09-184-001-3	Sequence 3, Appl1
c	34.6	1.8	4450	3	US-08-617-860B-2	Sequence 2, Appl1
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42	34.2	1.8	4383	6	5177307-1	Patent No. 5177307
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c	34	1.8	5829	4	US-09-439-313-473	Sequence 473, App

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/08485107
; Patent No. 5767376
; GENERAL INFORMATION:
; APPLICANT: STILES, JOHN I.
; APPLICANT: NEUPANE, KABI R.
; TITLE OF INVENTION: ACC SYNTHASE GENE AND ITS USE IN PLANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,107
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UH-01170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1888 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 17..1480
US-08-485-107-1

Query Match 38.2%; Score 735; DB 1; Length 1888;
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Db 1182 TAAACGAAATAAATAACTCAATGTATCTCTGGTTCGTCTTCCACTGCTCAGAACCTGGCT 1241
QY 1319 ggtttaaggggtgctatgccacaactggatgatggctgtgcaaatgtcttgcacgaa 1378
Db 1242 GGTTCAGGGTTCGTTTGCAACATGACGATAGACAAATGGAATTCACATGTCAAGAA 1301
QY 1379 tcgcgaacttgcgtcttcaaaaacaaaggaggtcgtggtcgtcgaataaagaacattgttggc 1438
Db 1302 TCAAAACCTTCATGCTTCAACATAAGGAAGCAATGGTGCCTAAAAAGAAACTTTGCTGGC 1361
QY 1439 acagtaacttgaggtgagcctc-----aaaccagaaggtttgatgata 1483
Db 1362 AAATAGTCTTAGACTCAGCTTCTCCTCGCTATGAGGATATCATGGAGACACCGGGTT 1421
QY 1484 tcacatgtcacctcactctccctcactcactcagtcacactatggttaagcca 1534
Db 1422 CGTTCATGTCTCCTCCTACTCGCTTATACCTCAATCACTCTTGTTCGAGCCA 1472

RESULT 2
US-08-724-194-3
; Sequence 3, Application US/08724194
; Patent No. 5824875
; GENERAL INFORMATION:
; APPLICANT: RANU, RAJINDER S.
; TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
; TITLE OF INVENTION: IN GERANIUMS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SANTANGELO LAW OFFICES PC
; STREET: 315 WEST OAK STREET, STE 701
; CITY: FORT COLLINS
; STATE: CO
; COUNTRY: USA
; ZIP: 80521
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,194
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTANGELO, LUKE
; REGISTRATION NUMBER: 31,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 224-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-724-194-3

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	Query Match	35.7%	Score 686.4	DB 1	Length 1878
	Best Local Similarity	70.8%	Pred. No. 1e-199		
	Matches 1001	Conservative	0	Mismatches 396	Indels 17
				Gaps	6
Qy	107	accaaactcccttgttgcgaagatggctattggggatggacatggcgaatcatccccat	166		
Db	129	ACCAAGAACATTCTTATTAAGATGGCACTGGAGATGGACATGGCGAANAACACCTT	189		
Qy	167	actttgatggatggaaggcttatgatcaaaaccccttctatccccacagataatctctaagc	226		

189 ACTTTGATGGCTGGAAGCTTACGACACACATCTTCCATCTCCCCAAACCCCTCAAG 248
227 gtgttgcaaatgggtgttctgagaaatcagcttaccctctgatttgggttgaagattgga 286
249 GTGTCATCCAGATGGGCTCGCAGAAAATCAGCTTCTTTCGAGTTGATTGAGCAANTGG 308
287 tactgaacaacccitgaagctccatttgcactccagaagaataaattatcaggggcca 346
309 TCCTTACAAACCCCAAGCCYCCATTTGCACAGCAGCAAGGTCGCAAGAAATCAAGGACA 368
347 tagctaaacttcaggattatcatgtctggccgagttcagaaatgctg-tgctaaattt 405
369 CTGCAATCTTTCAAGATTACCATGG-CTTGAGAGTTTCAGATATGCTTTTGCRAATTC 427
406 atggtctagaacaaggggaaacagaataocgtttgacctgcacctgatttgcattgagcgtt 465
428 ATGGGAAGGTTGAGAGGAACAGAGTAACTTTAACCCAGATCGCATAGTTATGAGTGA 487
466 ggaaccaccggagcacacgaagtcactgctcttttggtcagatcccgcgagggcattc 525
488 GGAGCACTGGAGCTCATGAATGATTCCTTCTGTTGGCTGATCTCCGCGATGCTTTT 547
526 ttatgcccattccctattatccaggctttgaccgggatttggagtgagacacaggatt 585
548 CTGTCCTCAACTCTTATTATCTCGGATTTGATAGACCTGAGGTGGAGAACTGGTGTG 607
586 aaacttggcc---agttatgctgcatagctcacaataatttcgtgttgacaaaagaa 642
608 CAGCTAATCTCTAGTAGTAGTCTGTGAAAGTGAAACAAATTTTCAGATCACCCGAAGTCC 667
643 ttggaagatgcctatgagaagaagaagagagataacatcagagtaaaaggtttactgac 702
668 TTAGAAGAGCTATGAGAGAGCTCAAGAGGACAAAGATTAGAGTCAAGGGATTGCTCATA 727
703 accaatcataatcattatgacacatcattgacagagaagacactgagaccgtggtg 762
728 ACAAACCCATCAACCCACTAGGAACTATCTCTGGACAGAGACACTAGTCAGTCTAGTG 787
763 agcttcataatgagaagcgtatccactgtgtatgtatgataaataatgctgcacacggtt 822
788 AGCTTTCATCAATGAAAGAAACATTCACCTTGCTGTGATGAATCTACGCCGCCACAGTC 847
823 ttcaagcaaacccgtttcataagaatagctgagatattagaggatgaaacagacatagag 882
848 TTTCTCTCAGCCCGCTTCTGTTAGCATTTGCTGAGGTTATCGAGCAAGAGA---ACGTTTCG 904
883 tgtgaccgcacacctcgtacacattgtttatagctcttcaagagacatggggttccctggc 942
905 TGCAACCGGACCTCATCCACATTTGCTACAGCCTGTCCAGGACATGGGTTCCCTGGC 964
943 ttcaagagtcggcactatatactctacaatgatgctgtggttaattgtgcacgcaaaatg 1002
965 TTCAGGGTGGGATTTCTACTCTACAAATGACGACGTTGTGAATTTGCGCGAAGATG 1024
1003 tcaagctttggattggtgtcaaacacagactcagtatottttagcatcgatgctgctaaatgat 1062
1025 TCAAGTTTCGGCTTGTATCCACACAAACTCAGCACCTAATCGCATCAATGCTCTCGGAC 1084
1063 gatgagttgtggagaggtttctgagagagtgacaaaggttggctcaaggtttcagg 1122
1085 GATGAATTCGTGGACATTCATCTGCTGAGAGCGGAGGAGGCTAGCGAGAAAGGTACACA 1144
1123 gtttcaactgggggttggccaaagtggcataaagtgtcttgcaagcaaatgctggttcta 1182
1145 ACCTTCACAAAGAGGCTTGACAAAGTGAACATTTGGATGCTTAAGAGCAATGGGGGTTA 1204
1183 ttgtgtgagatgatttaaggcaacttctcaaaaagccaaacttctcgactctgaacaggag 1242
1205 TTATATGATGGATGGACTTTGAGAGGGCTTCTCAAGGAGAAGACTTTTCGAGGGCGAGATGCT 1264
1243 ctttgaagaattatcattcatgaattgaagataagataatttccactggctattcctccat 1302

Db 1265 CTGTGGAGAGTGATTAATCAATGAAGTGAAGCTAAATGTCTGCCAGGGCGTGTTCAT 1324
Qy 1303 tgcactgagccagggtggttaggtgtgctatgccaacatgatatgatatggtgtgcaa 1362
Db 1325 TGCTGGAGCCAGGGTGTGTAGAGTGTGCTTTGCCAACATGATGACTTGCAGATGCAG 1384
Qy 1363 attgctttgcaaacgaatccgcgaactttgtgcttcaaaaacgaagaggtgtggtgt----- 1417
Db 1385 GTGGCTCTCGAGGAGTATCAACATTTGCACTTTCAGAACAGGAAGCTCGGTTTTCCT 1444
Qy 1418 -ctaataagaacaattgtttggcacagtaactt---gagctgagcctcaaaacccagaag 1473
Db 1445 GCAATCAAGACACTGTGTGGCAAAACACCTTGAAGGCTCAGCTTGTCTTTCAGGAGA 1504
Qy 1474 ttgtgatataccactgtcaccctcactctcccc 1507
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RESULT 3
; Sequence 11, Application US/08695412B
; Patent No. 5874369
; GENERAL INFORMATION:
; APPLICANT: STILES, JOHN I.
; APPLICANT: MOISYADI, STEFAN
; APPLICANT: NEUPANE, KABI R.
; TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
; TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
; TITLE OF INVENTION: RIPENING OF COFFEE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JONES, DAY, REAVIS & POGUE
; STREET: NORTH POINT, 901 LAKESIDE AVENUE
; CITY: CLEVELAND
; STATE: OHIO
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS v. 5.1
; SOFTWARE: WordPerfect v. 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,412B
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/485,107
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRIFFITH, CALVIN P.
; REGISTRATION NUMBER: 34,831
; REFERENCE/DOCKET NUMBER: 265036600002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 586-7050
; TELEFAX: (216) 579-0212
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2040 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1653
; US-08-695-412B-11

Query Match 35.0%; Score 673.8; DB 2; Length 2040;
Best Local Similarity 68.0%; Pred. No. 7.6e-196;

Matches 974; Conservative 0; Mismatches 447; Indels 12; Gaps 2;

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QY 106 gacaaactcccttggttccaaagatgctattggtggaatgacatggaacatcatcccca 165
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Db 208 GAAACAAACAACTCTTGTGGAAGATGGCAACCAACGATGGCAATGGGAAATCGCCT 267

QY 166 tactttgatggaagcttatgatcaaaaccccttccacacagataaactcaac 225
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Db 268 TATTTGATGTTGGAAGCATATGATAGTATCCTTACCATTCCACAGAAATCCTAAT 327

QY 226 ggtgtatgcaaaatgggtcttgctgagaaatcagcttaacctgtattggttgaagattgg 285
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Db 328 GGTGTATATACAGATGGGACTCGCAAAATCAGTTATGCTTTGATTTGATCGAGGAATGG 387

QY 286 atactgaacaacctgaagctccatttgaactccagaaagaaataaattcaaggccc 345
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QY 346 atagtaactttcaggattatcatggttgcgcaggttcagaaatgctgtgctaaattt 405
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QY 466 ggaagccacggagcacacgaagtcaactgcttggcttggcagatcccgcgagccattc 525
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Db 568 GGGCAGACCGGAGCTCATGAACTCTGCGCTTCTGTTAGCTGACCCCTGAAGATGCGTTT 627

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Db 628 TTGTTACCCACCATATATCCAGGATTGATCGGATTTGAGTGGCGGCAACAGGATG 687

QY 586 aaactgttccagtatgtgcga tagtcaaaatattcgttggacaaaggaagcattg 645
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Db 688 CAACCTCTTCCAATTTGTCGAGCTCCAATGATTTAAGGTCACATAAAGAAATCCATG 747

QY 646 gaagatgctatggaagcaagagagataaactcagatgaaggtttactgatcacc 705
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 GAAGTCTCTATCAGAAAGCTCAGAAAGCCACATCAGATGAAGGGGTTCCCTTTAAAT 807

QY 706 aatccataatccattagtcacaatcatgagacagaagacactggaacacgtggtgagc 765
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Db 808 AATCCATCAATCATTTGGAACTGTTCTTGACAGGGAATTTGATTGATATAGTCACA 867

QY 766 ttcataatgagaaggtatccacctgtatgtgataatataatgtcgaacagtttc 825
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Db 868 TTCATCAATGACAAAAATATCCACTTTGATTTGTGATGAGATATATCTGCCACCGTCTC 927

QY 826 agccaaacccggtttcctaagcatagctgagatattagagatgaacagacatagagtg 885
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Db 928 AGCCAGCCGAATTCATCAGCTCTGGAATTAATGAGCAT-----GATGTTCAATGC 981

QY 886 gaccgcaacctgtcacacattgttttagtctttcaagagacatgggttccctgcttc 945
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Db 982 AACCGTGATCTATACATCTTGTGTATAGCTGTCCACAGACTTGGCTTCCCTGGATTC 1041

QY 946 agagtgcggatcataactcttacaatgatgtgtgttaattgtgcacgcaaaatgtca 1005
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Db 1042 AGAGTTGGCATTTTGTATTATATAATACGCTGTGTGTCAGCTGTCTAGAAAAATGTGC 1101

QY 1006 agcttttgattggtgtcaacacagactcagatcttttagcatcgatgataatgatgat 1065
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Db 1102 AGTTTCGGCTGTTTTCACACANACTAGCATCTGATTGCTCAATGTTATCGGACGAA 1161

QY 1066 gagtttggagaggtttcttgcagagagtgcgaagaggttggctcaagggttcagggtt 1125
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Db 1162 GCATTTATGGACAAAATCATTTCCAGAGCTCAGAGAGATTAGCTCAGGAGGATGCTTT 1221

QY 1126 ttcactgggggttggccaaagtggcataaagtgtcgttcaagcaaatgctgtgtattt 1185
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Db 1222 TTCACAAAGAGGACTTGTCTCAAGTAGGCATTTGGCACCTTAAAAAGCAGTGGCGGCTTTAT 1281
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RESULT 4

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US-09-043-627-9
; Sequence 9, Application US/09043627
; Patent No. 6124525
; GENERAL INFORMATION:
; APPLICANT: Botella, Jose Ramon
; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MATHIWS, COLLINS, SHEPHERD & GOULD P.A.
; STREET: 100 Thonet Circle, Suite 306
; CITY: Princeton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08540-3662
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,627
; FILING DATE: 20-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00591
; FILING DATE: 20-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN5559
; FILING DATE: 20-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN9603
; FILING DATE: 02-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernstein, Scott N.
; REGISTRATION NUMBER: 38,827
; REFERENCE/DOCKET NUMBER: 3573-11US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-924-8555
; TELEFAX: 609-924-3036
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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QY 1186 gtgtgatgatttaaggcaactctcaaaaagccaaactctgactctgaaacggagctt 1245
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1282 TTCTGGATGGACTTAAGGAGACTCTCAGGGAGTCCACATTTGAGGCAGAAATGGAACTT 1341

QY 1246 tggaaagtattatcatcgaagttaagatcaatgtttcaacctggctattccctccattgc 1305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1342 TGGAGGATCATATAATACATGAAGTCAAGCTCAATGTTTCCACAGGCTTATCTTTCCATTGC 1401

QY 1306 actgagccagaggtgttttaggtgtgctatgccaacatgagatgatatggctgtgaaaaatt 1365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1402 TCAGAACACAGGATGTTTCTGAGAGTTTGGCTTTGCCAACATCGACGACGAAAGTGTGAGAGTT 1461

QY 1366 gctttgcaacgaactcgcgaactttgtcttcaaaaacaaaggaggtcgtgtg-----tct 1419
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Db 1462 GCTCTCAGAAGAATCCACAAATTTGTCTGTTCAGGGCAAGGCACAGACGCAACAAC 1521

QY 1420 aataagaacaattgttgccacagtaactgaggtgagcctcaaaacacagaaggtttgat 1479
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Db 1522 CCAAAGAGTCTGCTGGGAAAGCAGCAAACTTCAACTCAGCTTATCTTTCCGCAGATTGGAC 1581

QY 1480 gatatacaccatgtcacctcacctctccctcacctcagtcacacctatggttaaaagc 1532
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Db 1582 GAAAGGTGATGGGATCGCATATGATGATGCTCCCTCACTCCCGATGGTCTCAC 1634
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FEATURE: 33.0%; Score 635.2; DB 3; Length 1113;
Best Local Similarity 74.3%; Pred. No. 3.4e-184;
Matches 831; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 235 caaatgggtctgtgagatcagctaccctctgattggttggaagattggatactgaac 294
Db 1 CAGATGGGATTTGGGGAAATCTGCTTTGCTTTGATTAGTTCAAGAANTGGGCTTAAGC 60

QY 295 aaccctgaagcctccatttgcactccaggaaggaataaattgattccagggccatagctaac 354
Db 61 AACCAGAAAGCCCTCTATCTGCACCTGCCGAAGGTATAAGTCAATTTTCAGAGATATCGCTATC 120

QY 355 ttccaggattatcatggtctgcccaggttcagaaatgctggtctaaatttggctaga 414
Db 121 TTTTCAGGATTTACACGGCTTGGCAGAGTTTCAGAAATGCTGTTCAAATTTTATGGCAAGA 180

QY 415 acaaggggaaacagaaatcctgttaccctgaccgctattgtcatgacggtgagccacc 474
Db 181 GTGAGAGGAATAGAGTCAATACGACCTGATCGAATTTGTTATGAGCGTGGAGCAACC 240

QY 475 gagacacaggaagtcactgccttttgttggcagatcccgggagagcattcttagtgcgc 534
Db 241 GGAGCACATGAGACGGTTCCTTTGCTGCTGATCCCGGTGAAGCATTTTGGGTGCG 300

QY 535 attccctattatccagccttttgaacgggattgagtgagacagagattaaacttgt 594
Db 301 ACTCCTTACTATCCAGGATTTGGTCGAGATTTGAGATGGAGAACAGGAGTTCAACTTTT 360

QY 595 ccagttatgctgagatgcataataatttcgtgtgacaaaaggaacattgggaagtgc 654
Db 361 CCAGTTGTGTGACAGTTCTAACATTTCAAGATTACAAGAGAACCGGTGGAAGCAGCA 420

QY 655 tatgagaagcagagagagataacatcagagtaaaaggttactgatacccaatccatca 714
Db 421 TATGAAAAAGCTCAAGAAACACATTCAGAAATCAAGGGTTTGGTCTCCACAAATCCATCG 480

QY 715 atccattagccacatcatgacagaaagacactgagaaacggtgtagcttcatcaat 774
Db 481 AACCCGCTGGGACTTGTGTCACAGAGAAACATTAAGAAGTTTGTAGAGCTTCATTAAT 540

QY 775 gagaagcgtatccacctgtatgtgatgaatatatgctgcaacagttttca---gccaa 831
Db 541 GAAAGAACATCCACTTAGTCTGCGACGAGATTATGCTGCCACATCTTCATGGGCCAG 600

QY 832 cccggtttcataagcagtagctgagataattagaggatgaaacagacatagagtgtgaccgc 891
Db 601 CCGGATTTTCATTAGCATCTCTGAAATTTATAGAAGTTCAGATTTCACTGCAATCGC 654

QY 892 aacctgacacattgtttatagctcttcaaaaggacatgggttccctgagcttcagagtc 951
Db 655 ATCTCATCCACTCTGTTTACAGTCTTTCAAGGATCTGGGGTTCCAGGCTTTAGGGTC 714

QY 952 ggcatacatactcttaccatgatgctgtggttaattgtgacgcgcaaaatgtcaagcttt 1011
Db 715 GGCATTATATACATACACAGATACAGTTGTGAGTTGCGCTGCACAAATGTCAAGCTTT 774

QY 1012 ggttggtgtcaacacagcagcagtcagtattcttttagctatcgatgctaaatgatgatgagttt 1071
Db 775 GGACTTGTATCATCAAAAATCAAACTTAATGCTTCAATGTTATCAGATGATGAATTT 834

QY 1072 gtgagagattttctgcaagagtgcaaaaggttggctcaaaaggttcagggttttcaact 1131
Db 835 GTGATAGGTTCATTTACTGAGAGTGTCTAAAGGCTTTGCAAAAGGCACAGAGCCTTCACA 894

QY 1132 ggggggttggccaaagtgtggcataaagtgtcttgcaaaagcaatgctgtcttattgtgtg 1191
Db 895 TGGGGGCTATCTCAAGTAGGCATTGTTGTTGAGAGCAATGCGGGGCTATTTTCTGG 954

QY 1192 atggatttaaggcaactcttcaaaaaaaccaactctctogactctctgaaacggagagctttggaaa 1251
Db 955 ATGATTTGTCATCATCTCTCTCAAGGAGCAAACTGATGAAGCAGAGATAGAACTGTGGAAA 1014

QY 1252 gttatcatcatgaagttaagatcaatgttttccacctggctattcttccattgcactgag 1311
Db 1015 GTGATTAATCAACGAAGTTAAATTAATGTTTCTCCGGGTTCTTCCCTTTTCATTCGCGCTAAT 1074

QY 1312 ccagggtgggtttaggtgtgctatgccacatggtatga 1349
Db 1075 CCAGGATGTTTCGGGTTGTTTCGCCAACATGGACGA 1112

RESULT 5
US-08-378-313-24
; Sequence 24, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; NUMBER OF INVENTIONS: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..1545
US-08-378-313-24

Query Match 32.8%; Score 630.2; DB 4; Length 2230;
Best Local Similarity 65.4%; Pred. No. 1.7e-182;
Matches 961; Conservative 0; Mismatches 493; Indels 15; Gaps 2;

QY 51 acctttttacactccacactcttaaccacatacacatggttgcagggccatggacca 110
Db 54 AATTTCTTCACTTCTAACTATTTAGTAAAAAATGGGATTTGAGATTTGCAAAAGAC 113

QY 111 aactccctgtttgtccaaagatggctattggggatggacatggcgaatcatcccaactt 170

Db 114 CAACTCATCTTATCAAAATTTGGCTACTAATAAGAGAGATGGCGAAAACTCGCCCATATTT 173
Qy 171 tgaatgaggaaggtctatgacaaacccctttcatccacagataatcctaacgggtg 230
Db 174 TGATGGTGGAAAGCATACGATAGTAGCTTTCCACCTCTAAAAACCCCAACGGAGT 233
Qy 231 tatgcaaatgggtctctgtgagaaacagctctacctctgatttggttggaagtact 290
Db 234 TATCCAAATGGGTCTGTCTGAAATCAGCTTTGTTTAGACTTGATAGAGATTGGATTAA 293
Qy 291 gaacaacctaaagccctcattctgacccagagaagaataatgattcagggccatagc 350
Db 294 GAGAAACCCAAAGGTTCAATTTG---TTCGAAGGAATCAATTCATCAGGCGCATTTGC 350
Qy 351 taacttcaggattatcatggtctgcccagttcagaatgctggtggtctaaatttatggc 410
Db 351 CAACCTTCAAGATTATCATGCTTGCCTGMAATTCAGNNAANGGATTGCGNAATTTATGA 410
Qy 411 tagaacaaggggaaacagaaatcaactgttgacccctgacccgtattgtcatagcggtagc 470
Db 411 GAAACAAAGAGGGAAGAGTTAGATTGTATCCAGAAAGAGTTGTATGTTGGTGGTGC 470
Qy 471 caccgagacacagagtcactgcctctttgtttggacatcccgcgaggcatctctagt 530
Db 471 CACTGGACTAATGAGACAAATATATTTGTTGGCTGATCCTGGCGATGCAATTTTATG 530
Qy 531 gcccatccctattatccaggctttgaccggatttgagggtgagaaacagagttaaaact 590
Db 531 ACCTTCACCATATACCCAGCATTTAACAGAGATTTAAGATGGAGAACTGGAGTACAACT 590
Qy 591 tgttccagttatgctgtagctcaaaataattcgtgttgacaaagggaagcattggagga 650
Db 591 TATTCCAATTCACCTGTGAGCTCCAAATATTTCAAAATTAATCTCAAAAGCAGTAAAAGA 650
Qy 651 tgctcatgagaaacagagaggataacatcagagctaaagggtttactgatcaccaatcc 710
Db 651 AGCATATCAAAATGCAAAAATCAAAATCAAAATCAAAATGAAAGTTTGATTTGACCCATCC 710
Qy 711 atcaaatccattaggacaaatcatggacagaaagacactgagaaacggtggtgagcttcat 770
Db 711 ATCAAAATCCATTTGGCACCACCTTTGGACAAAGACACACTGMAAAGTGCTTGAGTTTAC 770
Qy 771 caatgagaaaggtatccacctgtgtgtagtgaataatactgctgcaacagttttcagcca 830
Db 771 CAACCAACACAAACATPCCACTGTGTGTGACGMAATCTACGCGACCACTGCTTTTGACAC 830
Qy 831 acccggtttcataagcatagctgagattatagaggatgaacacagacatagagtgtagccg 890
Db 831 GCCTCAATTCGTACATAGCTGAATCCTCGATGACAGGNAATGACTTACTGCAACAA 890
Qy 891 caacctgacacattgtttatagctcttcaaaagacatggggttccctggcttcagagt 950
Db 891 AGATTTAGTTACATCGTCTCAGTCTTTCAAAAGACATGGGTTTACCAGGATTTAGAGT 950
Qy 951 cggctatataactcttcaaatgactgctggtggttaattgtgcaacgcaaaatgtcaagtt 1010
Db 951 CGGAATCATATATTTTAAACGAGATGCTGTTAATTGTGCTAGAAAAATGTCGAGTTT 1010
Qy 1011 tggattggttcaacacagactcagatcttcttttagcatgctgactaaatgatgatgagt 1070
Db 1011 CGGTTAGTATCTACACAAACCAATATATTTTACGGCAATGCTTACGGACGAAAAAT 1070
Qy 1071 tgtggagaggtttctggcagagtgcaaaagaggttggctcaaaaggttcagggttttccac 1130
Db 1071 GCTCGATAATTTCTAAGAGAAAGCGCATGAGGTTAGGTAAAGGCGCACAAACATTTTAC 1130
Qy 1131 tggggggttgccaaagtggcataaaagtcttgcaaaagcaatgctggtctatttgggtg 1190
Db 1131 TAATGGACTTGAAGTAGTGGGAATTAATGCTTGAATAATTAATGCGGGGCTTTTGTGTG 1190
Qy 1191 gatggattgaaggaactcttcaaaagcccaactctgactctgaacggagcgtttggaa 1250
Db 1191 GATGGATTGGCTCCACTTTTAAAGGAATCGACTTTTCGATACCGGAAATGTCGTTATGGAG 1250

Qy 1251 agttatcatcatgaagtttaagatcaaatgtttcacctggctattccttccattgcactga 1310
Db 1251 AGTTATATAAAGATGATTAAGCTTAACGCTCTCGCTGGATCTTCGTTTGAATGTCAAGA 1310
Qy 1311 gccaggggtggttaggggtgctatgccaacatgatgatataggctgtgcaaatgcttt 1370
Db 1311 GCACGGGTGTTCCGAGTTGTTTTCCAAATATGGATGATGGAACGGTTGATATTGCGCT 1370
Qy 1371 gcaacgaatccgcaacttgg-----gcttcaaaacaaggaggtcggtgctc 1418
Db 1371 CCGGAGGATTCGGAGGTTGCTAGGTGTTGAGAAAGTGGAGATAAATCGAGTTCGATGA 1430
Qy 1419 taataagaaacattgttggcagcagtaacctgaggtcctcaaaacacagaggtttga 1478
Db 1431 AAGAAGCAACAATGAAGAAGTAATTTGAGACTTAGTTTTCCAAAAGAAATGTATGA 1490
Qy 1479 tgatatoccatgctcacctcacctccccc 1507
Db 1491 TGAAGTGTGTTTGTCAACACTTTCGTCTAC 1519

RESULT 6
US-07-809-457A-8
; Sequence 8, Application US/07809457A
; Patent No. 5512466
; GENERAL INFORMATION:
; APPLICANT: Klee, Harry J.
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Monsanto Co. BBAF
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/809,457A
; FILING DATE: 19911217
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,440
; FILING DATE: 26-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10538)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1800 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-07-809-457A-8

Query Match 32.6%; Score 627; DB 1; Length 1800;
Best Local Similarity 65.3%; Pred. No. 1.4e-181;
Matches 959; Conservative 0; Mismatches 495; Indels 15; Gaps 2;
Qy 51 acctttttacactccacactctaaacacatacacatatgggttttcaaggccatggacca 110

Db 117 AATTCTTCACTTCTAACTCATTTAGTAAATAAATAATGGATTTGAGATTTGCAAGAC 176
QY 111 aactcocttggttccaaagatggctatttggggatggacatggcgaaatcatcccccactt 170
Db 177 CAACTCAATCTTATCAAAATTTGGCTACTAATAAGAGCATGGCGAAATCGGCATATTT 236
QY 171 tgaatgaggaagccttatgatcaaaacccctttcccccacagataaatcctaacggtgt 230
Db 237 TGATGGTGGAAAGCATACCATAGTATCCTTTCCACCCCTCTAAAACCCCAAGCGGAGT 296
QY 231 tatgaaatgggttcttgctgagaatcagcttaccctctgatttgggtgaagatggatact 290
Db 297 TATCCAAATGGGCTTGCTGAATAATCAGCTTTGTTAGACTTGTATAGAAATGGATTA 356
QY 291 gaacaacctgaagcctccattgcactccagaaggaataaattgatttcaggccatagc 350
Db 357 GAGAAACCCAAAAGGTTCAATTTG---TTCTGAAGGAATCAAAATCATTAAGGCCATTCG 413
QY 351 taactttcaggattatcatgctgtgcccaggttcagaaatgctggtcaaaatttatgac 410
Db 414 CAACTTTCAAGATATATCATGGCTTGCTGAATTCAGAAAAAGCATTCGGAATTTATGGA 473
QY 411 tagaacaaggggaaacagaaatcagtttgacctgacctgattgctgacgctggagc 470
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QY 531 gccattccctattatccagcctttaccgggatttgaggtgagagacagagttaaact 590
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QY 651 tgctatgagaagcgaagagagataacatcagagtaaaaggggttactgatacccaatcc 710
Db 714 AGCATATGAAATGCAAAAATCAACATCAAAATCAAAAGTAAAGTTGATTTGACCAATCC 773
QY 711 atcaatccattagcacatcatgacagacagacacactgagacacgctggtgacttcac 770
Db 774 ATCAATCCATTTGGCCACCACTTTGGCAAGACACACTGAAAAGTCTCTGAGTTTTCAC 833
QY 771 caatgagaagcgtatccaccttgatgataaataatgctgcaacagttttcagcca 830
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QY 831 acccggtttcacaagcatagctgagatattagaggatgaaacagacatagagtgtgaccg 890
Db 894 GCCTCAATTCGTAGTATAGCTGAAATCCCTCGATGAACAGGAAATGACTTACTGCAACAA 953
QY 891 caacctgatacatggtttatagcttttcaaggacatgggttccctggttcagagt 950
Db 954 AGATTTAGTTTCACTGCTTACAGTCTTTTCAAAAGACATCGGTTTACCAGGATTTAGAT 1013
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Db 1014 CGGAATCATATATCTTTAACGACGATGCTGTTAATTTGCTAGAAAAATGCGAGTTT 1073
QY 1011 tggattggtgtcaacacagactcagttattttagcatcgatcgtaaatgatgatggtt 1070
Db 1074 CGGTTTAGTATCTACAAAAACGCAATATTTTATGCGCAATGCCATCGGACGAAAAAT 1133
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QY 1131 tgggggggttggccaaagtggcataaagtgttgcaagcaatgctggtctatttgtgtg 1190

Db 1194 TAATGGACTTCAAGTAGTGGGAATTAATGCTTGAATAAATAATCGGGGCTTTTTGTTG 1253
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QY 1251 agttatcatcagaagtttaagatcaatgtttcacctggctattccttccattgcaactga 1310
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QY 1311 gccagggttggttttaggtgtgctatgccaaactgagatgctgtgcaaatgcttt 1370
Db 1374 GCCAGGCTGGTTCGAGTTTGTGTTTGAATAATGATGGAACGGTTGATATTGCCCT 1433
QY 1371 gcaacgaatccgcaacttgt-----gcttcaaaacgaagaggtcgtggtgtc 1418
Db 1434 CGCAGGATTCGGAGGTTTCGTAGGTGTGAGAAAAGTGGAGATAAATCGAGTTCGATGA 1493
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QY 1479 tgatatcaccatgtcacctcactctcccc 1507
Db 1554 TGAAGTGTGTTGTCACCACTTTCGTCAC 1582

RESULT 7
US-08-553-943-8
; Sequence 8, Application US/08553943
; Patent No. 5702933
; GENERAL INFORMATION:
; APPLICANT: Klee, Harry J.
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Monsanto Co. B44F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,943
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/809,457
; FILING DATE: 17-DEC-1991
; APPLICATION NUMBER: US 07/632,440
; FILING DATE: 26-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10538)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1800 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-553-943-8


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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
PCT-US91-09437-8

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Query Match 32.6%; Score 627; DB 5; Length 1800;
Best Local Similarity 65.3%; Pred. No. 1.4e-181;
Matches 959; Conservative 0; Mismatches 495; Indels 15; Gaps 2;

Qy	51	acttttttacactccacactctaaocaaatacacccatatgggtttccaagggccatggacca	111
Db	117	AAATTTCTTCACTTCTAAACTCATTTTAGTAAAAAAAATGGGATTTGAGATTGCAAGAC	176
Qy	111	aactccctgtgtccaagatagcctattggggatggacatggcgaaatcatccccatactt	170
Db	177	CAACTCAATCTTATCAAAATTTGCTACTAATGAAGAGCATGCGAANAACCTGCCATATTT	236
Qy	171	tgatggatggaagcgttatgatcaaaacccctttcatccacagataatcctaacggtgt	230
Db	237	TGATGGTGGGAAGCATACGATAGTGATCTTTCCACCTCTAAAAAACCACGGAGT	296
Qy	231	tatgcaaatgggtctgtcgtagaatacagcttacctctctgattggttgaagattgatact	290
Db	297	TATCCAAATGGGTCTTTGCTCAAAATCAGCTTTGTTTAGACTTGATAGAAGATTGGATTAA	356
Qy	291	gaacaacctgaagcctccatttgcactccagaagaataaaatgatttcaagggccatagc	350
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Qy	351	taactttcaggattatcatggtctgctggcagatgcagaaatgctgtggtctaaattatggc	410
Db	414	CAACTTTCAGATTATCATGCGCTTGCCCTGAAATTCAGAAAAAGGATTGCGAAATTTATGGA	473
Qy	411	tagaacaaggggaacagaaatcacgtttgacctgacctgacogtatgtcatgagcgtggagc	470
Db	474	GAAAAACAAGAGGAGGAAGATTAGATTGTTGATCCAGAAAGAGTTGTTATGCGTGGTGGTGC	533
Qy	471	cacggagcacagcagtcacitgcctttgtttgttgcaatccccggcgaggtctcttagt	530
Db	534	CATCGAGCTATGAGACAATTATATTTTGTGTTGCTGATCCTGCGGATGATTTTATGT	593
Qy	531	gcccatcctcattatccaggcttgaccgggattgacgggttgagggtggagacaggagttaaact	590
Db	594	ACCTTCACCATACTACCCAGCATTTAACAGAGATTTAAGTTGGAGACTGGAGTACAAC	653
Qy	591	tgttcagttatgtcgatagctcaaaataattctdgttgacaaggaagcattggaaga	650
Db	654	TATTCOAATTCATGTTGAGAGCTCCAATAATTTCAAAATTTACTTCAAAAGCAGTAAAAGA	713
Qy	651	tgctatgagaagcaagaggatatacatcagatgaaggtttactgatcaccaatcc	710
Db	714	AGCATATGAANATGCAAAAATCAACATCAAGTAAAGTTTGATTTTGACCAATCC	773
Qy	711	ataaatccattaggcacaaatcatggacagaagcacactgagaaacggtggtgagcttcat	770
Db	774	ATCAAAATCCATTGGGCACCACCTTGGACAAAAGACACACTGAAAAGTGTCTTGAGTTTCAC	833
Qy	771	caaagagaagcgtatccacctgtatgtatgaaataatgctgcaacagttttcaagcca	830
Db	834	CAACAAACAACAATCCACCTTTGTTGTGACGAAATCTACGAGGCATCTGTCTTTTGACAC	893
Qy	831	accggtttcaagcatagctgaatatagagatgaacagacatagatgtgaccg	890
Db	894	GCCTCAATTCGTGATGATAGCTGAATCTCGATGAACAGGAAATGCTTACTGCAACAA	953
Qy	891	caacctcgtacacattgttta tagtcttttcaaagacatgggttccctggcttcagagt	950
Db	954	AGATTTAGTTCATCGTCTACAGTCTTTCAAAAAGACATGGGTTTACCAGGATTTAGAGT	1013
Qy	951	cggcatcatactcttacaatgatgctgtggtttaattgtgaogcaaaaatgtcaagctt	1010
Db	1014	CGGAATCATATATCTTTTAAACGACGATGCTGTTAATTTGCTAGAAAAATGTCGAGTTT	1073

Qy	1011	tgattggtgtcaacacagactcaagtatctttagcatcgatgctaataatgatgatgagtt	1070
Db	1074	CGGTTTAAATCTACACAAACGCAATATTTTTTTAGCGCAATGCCATCGGACGAAAAATT	1133
Qy	1071	tgtgagagggttctggcagagagtgcaaaagaggttgctcaaaaggttcagggttttcac	1130
Db	1134	CGTCGATPAATTTTCTTAAGAGAAAGCGGATGAGGTTAGGTAAAAGGCCACAAACATTTTTAC	1193
Qy	1131	tgggggggtggccaaagtggcataaagtgcctgcacaaagcaatgcctgctctatttclgtg	1190
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Qy	1191	gatggatttaaggcaacttctcaaaagccaaacttcgactctgaaacggagctgttgaa	1250
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Qy	1251	agttatactcatgaagtttaagatcaatgtttcaoctggcttattcttccattgcactga	1310
Db	1314	AGTTATTATAAACGATGTTTAAGCTTAACGCTTCGCTTCGGATCTCGTTTGAATCTCAAGA	1373
Qy	1311	gccagggtgttttaggtgtgctatgccaaacatgatatgctgtgcaaatgtcttt	1370
Db	1374	GCCAGGTGGTTCGGAGTTGTGTTTGCAAAATATGATATGATGAACGGTTGATATTCGGCT	1433
Qy	1371	gcaacgaatccgcaactttgt-----gcttcaaacaaaggaggtcggtgtgc	1418
Db	1434	CGCGAGGATTCGGAGGTTCGTAGGTGTTGAGAAAAGTGGAGATAATTCGAGTTCGATGGA	1493
Qy	1419	taataagaacaattgttggcacagtaacttgtaggtcgtgagcttcaaacacgaaggtttga	1478
Db	1494	AAAGAAGCAACAATGCAAGAACAATAATTTGAGACTTAGTTTTCGAAAAAGAAATGATGA	1553
Qy	1479	tgataccaactgtcaacctcaactctccc	1507
Db	1554	TGAAGTGTGTTTGTCCACCACTTTTCGTGTCAC	1582

RESULT

US-08-724-194-2
Sequence 2, Application US/08724194
Patent NO. 5824875
GENERAL INFORMATION:
APPLICANT: RANU, RAJINDER S.
TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
TITLE OF INVENTION: IN GERANIUM
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
STATE: CO
COUNTRY: USA
ZIP: 80521
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2678 base pairs
TYPE: nucleic acid

	Matches	912;	Conservative	0;	Mismatches	456;	Indels	3;	Gaps	1
Qy	122	tgtccaagatggtctattggggatggacatgcgccaatacatcccaactactttgatgatgga	181							
Db	109	TGTCAAAGATTGCAACCAACGACGACACGCGAGAACTCCCCATATTTCGATGGTTGGA	168							
Qy	182	aggtttatgatcaaaacccctttcatccacagataatcctaaaggtgtttatgaaatg	241							
Db	169	AGGCTTATGACCGGTATCCGTTCCATCCGTCACGAATCCTTAACGGGTATTATCCAGATGG	228							
Qy	242	gtcttctgagaaLcagcttacctctgatttgggtggaattggatactgacaaccctg	301							
Db	229	GTTTAGCTGAANAATCAGCTTTCATCTGACTTGATTGAAGATGGGTGAGGTCCAAACCCAG	288							
Qy	302	aagcctccattgcaactccagaagaataaattgatttcaaggccatagctaactttcagg	361							
Db	289	AAGCCTCAATCTGCACCTCTTGAGGAGTTGCTAAGTTCAAGGACGTAGCTAACTTTTCAGG	348							
Qy	362	attatcatggtctggccggatctgaagaatgctgtggtctaaatttatggtctagacaaga	421							
Db	349	ACTACCATGGGCTGCTGGAGTTCAGGACACGCCGTGGTAAATTTATGAGCAGAGAAGGG	408							
Qy	422	gaacagaatacacgtttgaccctgaccgtattgtcatgagcgttgagccaccggagcac	481							
Db	409	CGGGAAGGTCACATTGTGATCCGACCGTGTGTCATGAGCGCGGACCGACCGGAGCCA	468							
Qy	482	acgaagtcaactgaccttttgggtggacatcccgcgaggcaattttagtgcctatccct	541							
Db	469	ACGAGCTCATCGTCTCTGTGTGGCAATCCCGGAGCGCTTCTCTTCCCATCTCCTT	528							
Qy	542	attatcaggctttgacccggatttggaggtggagaaacagagagtttaactgttccagtta	601							
Db	529	ATTATCCAGCAAAACGACCGTGCATCTGAGTGGCGAACCGGAGCTCAGATCATTCGGGTGC	588							
Qy	602	tgtcgtatagctcaaaataatttctgttgacaaaggagcatttgaagatgccttatgaga	661							
Db	589	ACTGCCACAGCTCCACCGTTTCAAGATAACGAGAGGGCACTAGAAAGATCATACGGCAC	648							
Qy	662	aagcaagagaggataacatcatgagtaaagggtttactgatcaccaatccatcaaatccat	721							
Db	649	AAGCACAAAGAACACATAAACGTAAAGCGTGTCTTTAACCAACCCATCGAACCTTC	708							
Qy	722	taggcacaatcatggacagaaagcatgagaaacgtggtgagcttcatcaatgagaagc	781							
Db	709	TAGGCACAAATCTCGACCGCGACACTCTCAAGAGCATCTGTCAGCTTGTCTCACCGACAACA	768							
Qy	782	gtatccaccttgatgtagaataatctgctgaacagttttcagccaacccggtttca	841							
Db	769	ACATCCACCTAGTCACTGACGAGAAATCTACGCCGCCACCGCTTTTCGCCGCCCGGAGTTCG	828							
Qy	842	taagcatagctgagatattagaggatgaacacagacatagagtgtaccgcgaacctcgta	901							
Db	829	TAAGCGTCTCGAAATCTCTCCAGAAATGGAGACACACACGTCGACACCCGACCTCATCC	888							
Qy	902	acaattgttta tagtctttcaagacatgggggttccctggttccagagtggtgcatcat	961							
Db	889	ACATCTGTATACAGCCTGTCTCAAGGACTTGGGCATGCCGGGTTCGGGTCTCGGATCTCGTGT	948							
Qy	962	actcttcaatgatgctgtgttaattgtgcacgcaaaatgtcaagtttggattggtgt	1021							
Db	949	ACTCATTTCAACGACGACGCTGCTATCTCTGCGCACCGGAAGATCTCGAGCTTTCGGGTGTGT	1008							
Qy	1022	caacacagactcagtaLcttttttagcatcgtactaaatgatgatgagtttgtggaaggt	1081							
Db	1009	CGACCCAGACGACGACCTTCTCGACGGATGCTATCCGACGAGCTTTCGTGGAGCGGT	1068							
Qy	1082	tcttggcagagagtgcaaaaggttggctcaaaagtttcaaggggttttcaactgggggttgg	1141							
Db	1069	TCCCTCGCGGAGAG---CGGAGCTTGGGGAGGAGCGACGGCGTGTTCACGAAGAGGGCTCG	1125							
Qy	1142	ccaagttggcataaaagtgttgcagaagcaatgctgtgtctatttgtgtggaigtatttaa	1201							
Db	1126	AGGAGTGTGGGATTTGGGTGTTTAAAGACACACCGGGGCTCTACTTCTGTGATGTGATTTGC	1185							

Query Match 30.3%; Score 582.4; DB 4; Length 1703;
Best Local Similarity 56.4%; Pred. No. 5.8e-168;

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RESULT 11
US-08-378-313-18
; Sequence 18, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378.313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..1489
US-08-378-313-18

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Matches 854; Conservative 0; Mismatches 426; Indels 6; Gaps 1;			
Qy	122	tgtccaagatggtctattggggatgacatggcgaaatcatcccccatacttttgatgatgga	181
Db	51	TCTCGAAGATCGCCCTCGACGATGGCATGGCGAGAACTCCCGGTATTTCGATGGGTGA	110
Qy	182	aggcttatgatcaaaacccccttctatccacacagataaactcaacggtgtttagcaaatgg	241
Db	111	AAGCTTACGATACAGCATCCGTTTCACCCCTGAGAAATAATCCTTTGGGTGTATTCAAAATGG	170
Qy	242	gtctgtgagaaatcagcttacctctgatttggttggaagattggatactgaacaacccctg	301
Db	171	CTTTAGCAGAAAATCAGCTTTCTTTGATATGATTGTGACTGGATAGAAAACACCCCTG	230
Qy	302	aagcctccatttgcactccacagaaggaataaatgatttcaggcccatagctaactttcagg	361
Db	231	AAGCTTCGATTTGTACACCGGAAGGACTTGAGAGATTCAAAAGCATTGCCAACTTCCRAAG	290
Qy	362	attataatggtctggtccgagttcagaatgctgtgtgtaaatatttattgctagaaacaagg	421
Db	291	ATTACACACGGCTTACAGAGTTTCGAAATGCAATTTGCAAAATTTATGGGGAAAGTAAGAG	350
Qy	422	gaacagaaatcagctttgaccctgaccgtattgtcatgagcgtgtgagaccaccgagcac	481
Db	351	GTGGGAGGTAANAATTCGACCCGAGTCGGATTGTGATGGTGCGGTGGACCGGAGGA	410
Qy	482	acgaagtcaactccctttgtttggcagatcccgcgagggcattcttagtgcacattccct	541
Db	411	CGGAACCCGTCATCTTTTGTGGCGGATCCGGGGATGCTTTTTTGGTTCTCTTCCCAT	470
Qy	542	attatccaggttttgcacgggttttgaggttgagaaacaggagtttaaaacttgttccagta	601
Db	471	ATTATGACAGGATTTGATCGAGACTTGAATGGCGAACACAGACACAAATAAATTCGGGTCC	530
Qy	602	tgtcgatagctcaaatatttcgtgttgacaaagagcattggaagatgcctatgaga	661
Db	531	ATTGCAACGGCTCGAATAACTTCCAACTCACAAGCGCCCTTAGAATAGCCTACAAA	590
Qy	662	aagcaagagaggataacatcagagtaaaaggttttactgatccaccatccatcaaatccat	721
Db	591	AGGCTCAAGAGGCCAACATGAAGTGAAGGTGTATAATACCAATCCCTCAAAATCCCT	650
Qy	722	taggcacaatcattgacagaaagacacactgagaaacggtgtgagcttcataatgagaagc	781
Db	651	TAGGCACAACGTCGACCGTGACATCTTAAACCCCTCGTCACCTTTGTGAATCAACACG	710
Qy	782	gtatccaccttgtatgtgataatatactgtgcaacagttttcagcccaacccggtttica	841
Db	711	ACATTCACTTAATATCGGATGAATATACTCTGCCACTGTCTTCAAGCCCCAACCTTCA	770
Qy	842	taagcatagctgagatatttagaggatgaacacagacatagagtgtgaccgcaacctcgtac	901
Db	771	CCAGCATCGCTGAGATTGT------TGAACAAATGGAGCATTGCAAGAAGGAGCTCATCC	824
Qy	902	acattgtttatagtttttcaaaaggacatgggtttccctggcttcagatcgcgcatcatat	961
Db	825	ATATTCTTATAGTGTGCAAGACATGGGCTCCCTCGTGGTTTTCGAGTTGGAATTAATTT	884
Qy	962	actcttacaatagctgtgtgttaattgtgcaacgcaaaatgtcaagcttttgattggtgt	1021
Db	885	ATTCATTACAAAGCATGCTGCTGCTCGCCGCTGCTCGGCAGATGTCGAGCTTCGGCCTCGTCT	944
Qy	1022	caacacagactcagtatctttttagcatcgatgcttaaaatgatgatgatttgttgagagagt	1081
Db	945	CGTCCAGACTCAACATTTGCTCGCGGCATGCTTTTCGGACGAGGACTTTTGTGCGACAAAT	1004
Qy	1082	tcttcgacagagatgcaagaggttggctcaaaagtttcagggttttctactgggggttgg	1141
Db	1005	TTCTTGGCGAGAACTCGAAGCGTGTGGCGAGAGCATGCAAGGTTCAAAAAGAAATTTGG	1064
Qy	1142	ccaaagtgtggcataaagtgttgcgaagcaatgctgggtctctatttgtgtgagtgatttaa	1201
Db	1065	ATAAAAATGGGGATCACTTCTTTGAACACGCAATGCTGGAGTTTGTGTGGATGGATCTAC	1124

Qy	1202	ggcaacttctcaaaaagccaacttttcgactctgaaacgagcttggaaaagttaatcattc	1261
Db	1125	GGAGGCTATTAAAGACCAAAACCTTCAAAGCTGAAATGGAGCTTTGGCGTGTGATATCA	1184
Qy	1262	atgaagtttaagatcaaatgtttcacctggctattctctccatctgcactgagccaggggtgt	1321
Db	1185	ATGAAGTCAAGTCAATGTTTCTCCTGGCTCATCCTTTTCATGTCACCTGAGCCAGGTTGGT	1244
Qy	1322	ttaggggtgctcatgcccaactgagatgatgtgctgcaaatgtcttggcaacgaatcc	1381
Db	1245	TTGAGTTTGTTCGAAACATGGAGCACACACCGTTGACGTTGCTCTCAATAGAAATCC	1304
Qy	1382	gcaactttgtgcttcaaaaacaaggag	1407
Db	1305	ATAGCTTTGTCGAAAACATCGACAAG	1330

RESULT 12
US-08-632-598-1
; Sequence 1, Application US/08632598
; Patent No. 5886164
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: FLETCHER, JONATHON D
; TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABBY AND CUSHMAN
; STREET: 1100 NEW YORK AVENUE N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,598
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 223355/SPE50112/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 861-3000
; TELEFAX: 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1712 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: MUSA
; IMMEDIATE SOURCE:
; CLONE: ACS GENE
US-08-632-598-1

Query Match 29.7%; Score 571.4; DB 2; Length 1712;			
Best Local Similarity 64.1%; Pred. No. 1.3e-164;			
Matches 914; Conservative 0; Mismatches 501; Indels 12; Gaps 3;			
Qy	122	tgtccaagatggtctattggggatgacatggcgaaatcatcccccatacttttgatgatgga	181
Db	62	TCTCTCGATCCGACCAACGACGCCCATGCGGAGAACTCCTCTACTTCGATGGCTGA	121

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QY 182 aggtcttatgataaaaccccttccatcccccacagataatacctaaacgggtgttatgcaaatgg 241
DB 122 AGGCTTACGAGAGAGATCCCTTTCCACCTCACCGAACAACCCACCGGGGTTCATCCAAATGG 181
QY 242 gtcttgctgagaatcagcttaccctctgatgttggaagtggatgatactgaacaaccccg 301
DB 182 GACTCGCAGAAAACACAGCTTTCCCTCGACATTGATCCGAGACTGGATGAAGAAGAACCCAC 241
QY 302 aagctccatttgcaactccgaaggaaataatatttcaggggccatagctaaacttccagg 361
DB 242 AGGCTTCGATCTGCACCGAAGAAGGGGTCTCAGAGTTCAAAGCAATTCGCAACTTTTCAGG 301
QY 362 attatcatgtctgcgcgagttcagaataactgtggtggttaatttatgctagaacaagg 421
DB 302 ACTATCATGTCCTCCCAACCTTCGGAAGGCCATCGGCCCTGCTCATGGGAAGGTGAGAG 361
QY 422 gaaacagaatacagcttgacccctgacagctattgtcatgagcgggtggagccacggagcac 481
DB 362 GGGACGAGCCAGATTTGACCCACAGCCGATCGTGATGAGCGGTGGAGCCACCGCGCTC 421
QY 482 acgaagtcaactgcttttggcagatcccgcgagggtattcttagtgcccatccct 541
DB 422 AGGAACACATCGCCTTTTGGCTGGCTGATCTCTGGCGAGGCTTCTTGATTCCAAACGCAT 481
QY 542 attatccagcttgacgggatttgaggtgaggaacagaggttaaaacttgttccagtta 601
DB 482 ATTATCCGGGATTCGATCGAGATTCAGGTGGAGGACAGGAGTTTCAGCTCTCCCCATTC 541
QY 602 tgtcgatagctcaataattctgtgtgacaaaggagcattggaagatgcctatgaga 661
DB 542 ACTGCCACAGTTCCAAAGTTCAAGATCACCTTGGCGACACTGGAGACTGCTTACAGGA 601
QY 662 aagcaagaggagataaacatcagagtaaggggtttactatgatacccaatccatcaaatccat 721
DB 602 AGGCTGAAACTCACACATTAGAGTCAAGGAATACTTGGTGACCAACCCATCGAAACCCCTC 661
QY 722 taggcaaatcatgacagaagaacacatgagaacccgtggtagcttcatcaatgagaagc 781
DB 662 TGGCAACAACCATGGACAGAGACGCTGAGAACCCCTAGTCAGCTTCGTCAACGAGAAAA 721
QY 782 gtatccacctgtatgtgataataatctgctcaacagttttcagcaacccgggttca 841
DB 722 GGATGCACATTGGTGGACGAGATCTCTCCGAACCGTCTTCGACAGCCGAGTTACG 781
QY 842 taagcatagctgagatattagagatgaaacagacataagagtgtagccgcaacctgac 901
DB 782 TGACGCTCTCCGAGGTGATCGAGACGAGCCCTAC-----TGGCAGAGGATCTGATTC 835
QY 902 acattgtttatagctcttcaaggacatgggttccctggcttcagagtgcgcatcatat 961
DB 836 ACATCGGCTACAGCCTCTCCAAGGACCTGGCGCTCCCTGGCTTCGCGTCCGCGTCAAT 895
QY 962 actttacaatgactgtgtggttaattgtgcacgcaaaatgcaagcttttgattgtgt 1021
DB 896 ACTCTTACACGAGCGGTGTGAGCTGCGGAGGAGAGATGTCGAGCTTTGGACTGTCT 955
QY 1022 caacacagactcagatctttttagcatgagatgctgataatgatgatgtgtgtgagaggt 1081
DB 956 CGTGCAGACGACGCTCTCTGCTCTCCATGTTGGGAGACGAGGAGTTTCAACACGAGTT 1015
QY 1082 ttctggcagagagtcaaaagggttggtcnaagggttcagggttttcaactggggggttgg 1141
DB 1016 TCTTAGCGAGCGGACGAGGTTGTGCGGGCGGCGGAGGGTCTTTACGAGCGGCTCA 1075
QY 1142 ccaagttggcataaagtctgcaaaagcaatgctggtctatttgtgtgagatttaa 1201
DB 1076 AGCGAGTCGGGATTCATTGCTTGGACCGCAACGCGGGGCTGTTCTGCTGATGGACTTGA 1135
QY 1202 ggcaacttctcaaaagccaacttccagactctgaaacggagccttggaaagttatcattc 1261
DB 1136 GGCGGTGCTGAAGAAAGCAGCGGTGGAGCGGACGCTCGCGCTGTGGCGGTGATCATCA 1195
QY 1262 atgaagttaagatacaatgtttccactggctatttccctccattgcaactgagccaggggtt 1321
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Query Match 29.7%; Score 571.4; DB 4; Length 1712;
Best Local Similarity 64.1%; Pred. No. 1.3e-164;
Matches 914; Conservative 0; Mismatches 501; Indels 12; Gaps 3;

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DB 1196 ACGACGTGAAGCTCAACATCTCGCCGGGTGCTCTTCCACTGCTCGAGCCGGGTGGT 1255
QY 1322 ttagggtgtgctatgccaacatggtatggtgtgcaaatgtctttgcaacgaatccc 1381
DB 1256 TCAGGGTGTGCTTCCGCCAACATGGACGACGCGGCATGAAGATAGCGCTGAGGAGGATCG 1315
QY 1382 gcaactttgtg---cttcaaaaacaaggaggtcgtggtgtcttaataaagaacatgttggc 1438
DB 1316 AGATTTCGTGTACCGGAGAACGACGCGCTGTGCAAGCGCAAGAACAGAGAGGTGGG 1375
QY 1439 acagtaactgaggtgagctgagcctcaaaaccagaaggtttgatgat---atcaccatgtcac 1495
DB 1376 AGAAGCGCTGCGGCTGAGCTTGCTCGTGGAGGTTCGAGGATCCGTCCCATCATGACAC 1435
QY 1496 ctcactctccctcactcagtcacactatggttaaaagccacaaaattga 1542
DB 1436 CACATCTGATGTCCTCCACCATCGCCTCTCGTTCAGCGCCGCCACCTGA 1482
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RESULT 13
US-09-231-240-1
; Sequence 1, Application US/09231240
; Patent No. 6262346
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: FLETCHER, JONATHAN D
; TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY AND CUSHMAN
; STREET: 1100 NEW YORK AVENUE N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,240
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 861-3000
; TELEFAX: 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1712 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: MUSA
; IMMEDIATE SOURCE:
; CLONE: ACS GENE
; US-09-231-240-1

QY 122 tgtccaaagatgctctatttggggatgagacatgagcgaatcatccccactacttttgatgatgga 181
DB 62 TCTCTCGGATCGGACCAACGACGCGGCATGGGAGAACTCCTCTCTACTTTCGATGGCTGGA 121
QY 182 agcttatgatcaaaaccccttctatcccccacagataatcctaacaggtgttatgcaaatgg 241
DB 122 AGGCTTACGAGAGGATCTTCCACCTCACCAGAACCCACGCGGGGTTCATCCCAATGG 181
QY 242 gtctgtcagaaatcagcttacctctgatttggtagaatggaactggaactgaacacccctg 301
DB 182 GACTCGCAGAAAACACGCTTCCCTCGACTTGATCCGAGACTGGATGAAGAGAACCCAC 241
QY 302 aagcctccatttgactccagagaagaataaattgatttggggccatagataactttcagg 361
DB 242 AGGCTTCGATCTGCACGGAAGAGGGGTCTCAGAGTTCAAAGCAATTTGCCAACTTTCAGG 301
QY 362 attcatcagctgggcccagatgcagaatactgtgcttaatttatgctagacaagg 421
DB 302 ACTATCATGGCTCCCAACCTTCCGAAAGCCATGCCAGTTCATGGAGAGGTGAGAG 361
QY 422 gaacagaatcacgctttgacctgacctgattgtcatgagcgtgtgagccacccggagcac 481
DB 362 GGGGACGAGCCAGATTGACCCAGACCCGATCGTGATGAGCGGTGGAGCCACCGGGCTC 421
QY 482 acgaagtcactgcccctttgttggcagatcccccggcagacattcttagtgcacattccct 541
DB 422 AGCAACCATCGCCTTTTCCCTGGCTGTGATCCTTGGCAGGCTTCTGTATTCGAACGCCAT 481
QY 542 attatccagctttgacccggatttgaggtgagaaacagaggttaaaactgttccagttta 601
DB 482 ATTATCCGGGATTCGATCGAGACTTCAAGTGGGAGGACAGGAGTTTCAGCTCCCTCCCATTC 541
QY 602 tgtcgatagctcaaaataattctgtgttagcaaaagaaacattggaagatgcctatgaga 661
DB 542 ACTGCCACAGTTCCAAACAAGTTCAAGATCACCTTTGCCGCACTGGAGACTGCTTACAGA 601
QY 662 aagcaagagagataaacaatagagtaaaaggtttactgatcccaatcacaatccatccat 721
DB 602 AGGCTCGAAACTCACACATTAGAGTCAAAGGAATACTGGTGACCAACCCATCGAACCCCTC 661
QY 722 taggcaaatatgagacagaagacactgagaaccgtgtgagcttcatcaatgagaagc 781
DB 662 TGGGCACACCACTGACACAGAGACGCTGAGAACCCCTAGTAGCTTCGTCAACGAGAAAA 721
QY 782 gtatccaccttgtatgtgataataatatgctgcacagcttttccagccaccgggttca 841
DB 722 GGATGCACCTTGGTGTGCGACGAGATCTTCTCCGGAACCGTCTTCGACAAAGCCGAGTTAG 781
QY 842 taagcagctgagatatttagaggatgaaacagacagatagagtgtagccgcaacccctgtac 901
DB 782 TGAGCGTCTCCGAGGTGATCGAAGACGAGCCCTAC-----TGCACAGGGATCTGATTC 835
QY 902 acatgtttatagctttcaagagacatgggttccctggcttcagagtcgacatcatat 961
DB 836 ACATCGCTACAGCTCTCCAGAGACCTGGGGCTCCCTGGCTTCGCGTCGGCGGTCAAT 895
QY 962 actcttacaatgatgtgtgttgaattgtgcacgcaaaatgtcaagctttgtgattgggt 1021
DB 896 ACTCCTACAAACGACGCGGTGTGAGTGGCGGAGGAAGATGTCGAGCTTTGGACTGGTCT 955
QY 1022 caacacagactcagtatcttttagcatcagatgctaaatgatgatagttgttggagaggt 1081
DB 956 CGTCGACAGCGAGCTCTCTGCTCGCTTCCATGTTGGGACAGGAGGTTTCAACACGAGTT 1015
QY 1082 tcttgacagagtgcaagagagttggctcaaaagttcagggttttctactgggggttgg 1141
DB 1016 TCTTAGCGACGCGGACAGAGTTGTGGCGGCGGCGAGGCTTTACGGACGGCCTCA 1075
QY 1142 ccaaaagttggcataaagttcttgcaaaagcaatgctggtgtatttgtgtgattgatttaa 1201
DB 1076 AGCGAGTCGGGATTCATTGCTTGGACGGCAACGCGGGGCTGTCTGCTGATGGACTTGA 1135

QY 1202 ggaacttctcaaaagccaacttttgcactctgaaacggagcttggaaagttatcatc 1261
DB 1136 GGCCGTTGCTGAAGGAAGCGAGGTTGGAGCGGACCTCCGGCTGTGGCGGTGATCATCA 1195
QY 1262 atgaagtttaagatcaatgtttcacctggctattccttccattgcaagccaggggtgt 1321
DB 1196 AGAGCTGAAGTCTAACATCTCGCGGGGTCTCTTCCACTGCTCGGAGCGGGGTGT 1255
QY 1322 tttaggtgtgctatgcacaatggtatgctgtgtgcataattgtttgcaacgaatcc 1381
DB 1256 TCAGGGTGTGCTTCGCCAACATGGAGCACACGCCCATGAAGATAGCGCTGAGGAGATCG 1315
QY 1382 gcaacttttg---cttcaaaacaaggaggtgctgtgttctataagaacaattgttggc 1438
DB 1316 AGAGTTTCTGTACCGGGAGAACGACGCGCTCTGCAGGCGAAGAACAAAGAGAGGTGG 1375
QY 1439 acagtaacttgagctgagctcctcaaaacagaggtttgatgat---atcacatgtcac 1495
DB 1376 AGAAGCGTGGCGTGAAGCTTGCTCTGCTGCGGAGGTTCGAGGATCGTCCATCATGACAC 1435
QY 1496 ctcaactctccctacctcagtcacctatggttaaaagcccaaaattga 1542
DB 1436 CACATCTGATGCTCCCCACTCGCTCTCGTTCAAGCCGCCACCTGA 1482

RESULT 14
US-09-043-627-3
; Sequence 3, Application US/09043627
; Patent No. 6124525
; GENERAL INFORMATION:
; APPLICANT: Botella, Jose Ramon
; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
; STREET: 100 Thanet Circle, Suite 306
; CITY: Princeton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08540-3662
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,627
; FILING DATE: 20-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00591
; FILING DATE: 20-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN5559
; FILING DATE: 20-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN9603
; FILING DATE: 02-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernstein, Scott N.
; REGISTRATION NUMBER: 38,827
; REFERENCE/DOCKET NUMBER: 3573-11US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-924-8555
; TELEFAX: 609-924-3036
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

NAME/KEY: CDS
LOCATION: 1..1104
US-09-043-627-3

Query Match 29.7%; Score 571.2; DB 3; Length 1104;
Best Local Similarity 71.6%; Pred. No. 1.2e-164;
Matches 792; Conservative 0; Mismatches 308; Indels 6; Gaps 3;

QY 235 caaatgggttctgtgagaatcagcttaccctctgatttggtgaagattgatactgaac 294
DB 1 CAGATGGCCCTTGTGAGATCAGCTTGTCTTAAATTAATTCACGAGTGGCCGCTGAAA 60

QY 295 aacctgaagcctccatttcacccaagaaggaaataatttcaggggccatagctaac 354
DB 61 AACCCGAAGCCTCATTTGTACAAACAAGGAGCAGCTGAATTCAGAGATATAGCTATC 120

QY 355 ttccaggtattcatgtctgtggcgagttcagaaatgtctggctaaatttatggctaga 414
DB 121 TTTCAGATTTATCATGCTTGGCTGAATTCAGAGAGCTGTTCGAAAGTTATGGGAAA 180

QY 415 acaaggggaacagaatcacgtttgacccctgaacgttatgtcatgagcgtggagccacc 474
DB 181 GTGAGAAGAAACACAGAGCTTCAATTTACCCCTGATCGGATTTGTAGCTGGAGGACAACT 240

QY 475 ggagcacagaagtcactgcctttgtttggcagatccccggcaggcatcttagtgccc 534
DB 241 GGAGCTCATGAAATGATTTGTTTGTGCTGATCCTGGCGATGCTTGTGGTTCCA 300

QY 535 atccctattatccagcctttgacccggtattgaggtggagagcagagttaaactggt 594
DB 301 ACTCCTTATTTATCCAGGCTTTGTAGAGATTTGAGATGGAGACGGGAGCAAACTCAAT 360

QY 595 ccagttatgtcagatagctcaaatatttctgtgtgacaaaggaagcattgggaagatgcc 654
DB 361 CCAGTTCTGTGTAAGCTCAAAAGCTAACAGATTACAGATCACCATAGAACCCCTGGAGCTGCT 420

QY 655 tatgagaaagaagagaggaataacatcagagtaaaaggtttactgatccacaatccatca 714
DB 421 TATGAACCCGACAAAGAGTGATCATCAAGGTAAAGGTTTGTGTCATTAACCAACCCATCA 480

QY 715 aatccattaggaacaatcaggacagaaagacagacagcgtggtgagcttcatcaat 774
DB 481 AACCCACTGGGAACAATTTATCAAGGACACATTAGAACCTCTAGTCACTTCAACCAAC 540

QY 775 gagaagcgtatccacctgtatgtatgaataatatgct-gcaacagttttcagccaa-- 831
DB 541 CACAAGAAACATTCATCTGGTGTGTGATGAGATATATGCTGTTACCGTCTTCAGCCCAGG 600

QY 832 cccgggttcaatagcatagctagatattagagagatgaacacagacatagagtgaccgc 891
DB 601 GCCGAATTCACGACATAGCCGAGATAATTTGAAGAAGATA---AAATTTGTTGCAATCGT 657

QY 892 aactcgtcacacattgtttatagctcttcaagacatgggttccctgctgcagatgc 951
DB 658 GATCTCATCCACATCATTTACAGTTTATCCAAAGACATGGGATTCCTGGATTTAGAGTT 717

QY 952 ggcatactactcttacaatgatgtgtgtgttaattgtgcacgcaaaatgtcaagcttt 1011
DB 718 GGCATTGTGTTATCATACATGATGACGTGGTGTGAGTTGCTCGTAAGATGTCGAGCTTC 777

QY 1012 ggattgggtcaacacagactcagatctcttttagcactcagatgctaaatgatgatgatt 1071
DB 778 GGCTAGTATCTTCGCAAAACCCAGTATCTGATTGCTCCATGTTAGCAGACGATGAATTT 837

QY 1072 gtggagaggtttctgacagagtgcaaaaggttggctcaaaaggttcagggttttcaact 1131
DB 838 GTAGACAAATTTATTTGATGAGACGAAAGAGGCTGGCAATGACATAGATGTTTTTTCACA 897

QY 1132 ggggggtggccaaagtgtgcataaaagtctgtcgaagcaaatgctgctctattgtgtg 1191
DB 898 CAAAGACTTGTCAAGTAGGCATTAAGTGTGTTTAAAGCAATGCTGCTGTTGTTGTGGTGG 957

QY 1192 atgatttaaggcaactctcaaaaaaaccaacttctgactctgaaacggagctttggaaa 1251
DB 958 ATGATTTTGCCTAGACTGCTGAAAGAACACAGACTTTGAAGCAGAAATGCTGTTATGGAGA 1017

QY 1252 gttatcatcatgaagtttaagatcaatgtttcacctgagctattcttccattgcactgag 1311
DB 1018 GTAATTATAACGAATAAATACTCAATGATATCTCTGTTGCTGCTTTCCACTGCTCAGAA 1077

QY 1312 ccagggtggttaggtggtgctatgc 1337
DB 1078 CCTGGCTGGTTACGCGCTGCTGCTGCG 1103

RESULT 15
US-09-043-627-7
; Sequence 7, Application US/09043627
; Patent No. 6124525
; GENERAL INFORMATION:
; APPLICANT: Botella, Jose Ramon
; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
; STREET: 100 Thanet Circle, Suite 306
; CITY: Princeton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08540-3662
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,627
; FILING DATE: 20-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00591
; FILING DATE: 20-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PMS559
; FILING DATE: 20-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PMS603
; FILING DATE: 02-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernstein, Scott N.
; REGISTRATION NUMBER: 38,827
; REFERENCE/DOCKET NUMBER: 3573-1105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-924-8555
; TELEFAX: 609-924-3036
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1095
US-09-043-627-7

Query Match 29.5%; Score 567.8; DB 3; Length 1096;
Best Local Similarity 70.4%; Pred. No. 1.3e-163;
Matches 777; Conservative 0; Mismatches 317; Indels 9; Gaps 1;

QY 235 caaatgggttctgtgagaatcagcttaccctctgatttggtgaagattgatactgaac 294
DB 1 CAGATGGCCCTTGGCGAAGATCAGCTTGTCTTGTATTGATTCGGAAGACTGGATTTCGCAA 60

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 22:51:49 ; Search time 3456.34 Seconds

(Without alignments)

7509.286 Million cell updates/sec

Title: US-09-763-957-1

Perfect score: 1923

Sequence: 1 atctctctccacttactt.....aggcttcaatttcattcc 1923

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_estli:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	496.6	25.8	799	10	BI970666 GM830011A
2	486.8	25.3	578	9	BE020529 sm44h02.y
3	450.4	23.4	536	9	AW458572 sh10h02.y
4	396.2	20.6	651	10	BF649567 NF079G12E
5	388.6	20.2	507	10	BI974504 sal69d09
6	366.8	18.6	775	10	BM412805 EST587132
7	351.8	18.3	623	9	AW560294 EST315342
8	349	18.1	479	10	BM095045 saj25f06
9	344	17.9	630	10	BF650933 NF102B06E
10	336.2	17.5	766	10	BM410886 EST585213
11	334.8	17.4	653	10	BF648314 NF046D07E
12	323.4	16.8	672	9	AI898099 EST267542
13	322.4	16.8	468	10	BE555018 sp83902.y
14	321.2	16.7	575	9	AI484859 EST243120
15	316.2	16.4	819	10	BI421967 EST532633
16	314	16.3	573	9	AI165890 B003P14U
17	311	16.2	704	10	BI921823 EST541726

18	291	15.1	428	9	AV410488
19	290.6	15.1	632	10	BM404896
c 20	284	14.8	533	9	AW034048
21	281.6	14.6	658	9	AI487009
22	280.8	14.6	644	9	AI727528
23	280.2	14.6	373	9	AW102376
c 24	279.8	14.6	517	10	BI921101
25	276	14.4	628	9	AI727478
26	272.8	14.2	548	9	AI485016
27	271.4	14.1	361	9	AW781512
28	270.6	14.1	503	9	AI490629
29	269.6	14.0	618	10	BM110122
30	267.8	13.9	636	9	AI485332
31	267.6	13.9	595	9	AI897818
32	265.4	13.8	632	9	AI485399
33	265	13.8	831	10	BF272588
34	264	13.7	637	9	AW441375
35	259.8	13.5	585	9	AW618679
36	257.8	13.4	429	9	AV407744
37	251.6	13.1	564	9	AI490418
38	251.6	13.1	605	9	AI485635
39	247.4	12.9	513	9	AI487898
40	247.2	12.9	466	9	AI899645
41	247.2	12.9	583	9	AI731106
42	241.8	12.6	721	10	BG645853
43	241.4	12.6	749	10	BG600866
44	239	12.4	537	9	AI894662
45	237.2	12.3	462	9	AI488097

ALIGNMENTS

RESULT 1

BI970666/c

LOCUS

DEFINITION GM830011A11G11 Gm-r1083 Glycine max CDNA clone Gm-r1083-4149 3', linear mRNA EST 23-OCT-2001

ACCSSION BI970666

VERSION BI970666.1

KEYWORDS GI:16345071

SOURCE EST.

ORGANISM soybean.

Glycine max

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 799)

Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,

Expelding, J., Raph, C., Shoop, E., Pardini, J., Liu, L. and Lewin, H.

A Functional Genomics Program for Soybean (NSF 9872565)

Unpublished (1999)

Other ESTs: BE020529 corresponding to Gm-cl028-6796 (5')

Contact: Vodkin, L.O., PI, A Functional Genomics Program for

Soybean (NSF 9872565)

Lewin, H. A., Director, Keck Center for Comparative and Functional

Genomics

University of Illinois

Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA

Tel: (217) 244-6147

Fax: (217) 333-4582

Email: l-vodkin@uiuc.edu

This clone is available through: Incyte Genomics, 4633 World

Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or

(314) 427-3222 FAX: (314) 427-3324. Web site:

<http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio>

n/index

Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.

Location/Qualifiers

1. 799

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="Gm-r1083-4149"

/clone_lib="Gm-r1083"

/note="The library Gm-r1083 is a sequence-driven, rereacked set of 4,992 clones selected from cDNA libraries from various tissues and stages of development of soybean. It represents 1117 sequences from the progenitor library Gm-cl009 (from mature roots of 2 month old greenhouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-cl013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from library Gm-cl028 (from 'Supernod' plants whose seedlings were inoculated with Bradyrhizobium japonicum, courtesy of Dr. Gary Stacey). The 5' ESTs of the source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were rereacked to form library Gm-r1083. The cDNA clones of the rereacked Gm-r1083 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, <http://web.ahc.umn.edu/biodata/nsfsoy/>. Rereacking was performed by Incyte Genomics, St. Louis, <http://www.incyte.com>, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, <http://www.lie.uiluc.edu/biotech/keck.html>. Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."

BASE COUNT 256 a 168 c 139 g 215 t 21 others
ORIGIN

Query Match 25.8%; Score 496.6; DB 10; Length 799;
Best Local Similarity 81.3%; Pred. No. 3.3e-113;
Matches 642; Conservative 0; Mismatches 125; Indels 23; Gaps 6;

QY 1149 tggcataaagtcttgcaagcaatgctgtctatttggtagtggaattgaagcaact 1208
DB 799 TGGCATAAAGTGC-TGCAANNATNCTGTGCTCTTTGGTGTGATGATNAGGCAACT 741
QY 1209 tctcaaaaagcaactttcagactgaaacggagctttggaaagtatactcattcagaagt 1268
DB 740 NNTCAAGAACCCACGCTTGACTCTGAAATNNGNCTTTNNAAGAGTGCATGATGAGGN 681
QY 1269 taagatcaatgtttcactcggctattccctcattgcactgagcagggtgtttagggt 1328
DB 680 NAAATCATATGTTTCACTGGCTCCTCTTCCATTGCATGACAGCCAGGCTGTTNNGGT 621
QY 1329 gtgctatgccaacatggtatgctgctgctgcaaatgtgcttgcacacgaatccgcaactt 1388
DB 620 GTGCTATGCCAACATGGATGATGGCTGTGCAAAATTCGATTTGCAAGAATTCGTAACCT 561
QY 1389 tgtgtctcaaaaacaggaggtggtgtcttaataagaacatttggcacagtaactt 1448
DB 560 TGTGCTTCAAAAACAGGAGATCATGGTGCCTAACAGAACAATTTGTCACAGTAACCT 501
QY 1449 gaggctgagcctcaaaacagaggtttgatgatataccactgtcacctcactcctccct 1508
DB 500 GAGGTGAGCCCTCAAAACAGGAGGTGATGATATCATGATGATGATGATGATGATGAT 441
QY 1509 acctcagtcacactatggttaagccacacaaattgagttgtcattctcctcgaatgctta 1568
DB 440 ACCTCAGTCACCTCTGTTTAAAGCCACAAATTTGAGTTGSCATATTTCTCTGAACCCCTCA 381
QY 1569 gaagaagtaactgatgatggaagattacttgggtttctttttattttattttttggaaggtta 1628
DB 380 GAAGAAGTAACATGATATGATCATATTTTGGCTCTCTTTGACATGTTGTTTGGCAGGTA 321
QY 1629 cataa--gtgctggattgttttggaaacagcaataacacaggaattctctgatgtgttt 1686
DB 320 CATNAAGTCTGTGAGTTGTTTATTTTACACAGCAGTAACAGGCATGCTGTATATGTTT 261

QY 1687 tgtgatc-----ggcatcacatccagtgctcacaagtgtgtgctgcttcacgac 1737
DB 260 TTGTTACCAACATCCAAAGTCTCTTTGCCCTTGGCTATAGAACTTGTGCTACTGGAACAT 201
QY 1738 gcccttcaactttagggg-----catttttcttttttccacttaccacaa-----ggttc 1787
DB 200 GCCCCTTCAATTTTAGGGGCACTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 141
QY 1788 aaggtgaaaaaagtattatagatgctgtaattgtattgttttgcagaagagcccaaaaga 1847
DB 140 AAGGTGAAAAAAGTTATAGAGTTTGTAAAGGTTATTTGGTTTATTAGAGAGTCCGAAGA 81
QY 1848 tctctgtaactgctactgaaattgttaactttcaatttcaataatgaataatttataaagt 1907
DB 80 ACTCTGTATTCTTATACATGCAATTGTAA--GGTCGATGATCAATAAATTTGTTAATAGAGG 22
QY 1908 ctccaattc 1917
DB 21 NNTCAATAC 12

RESULT 2

BE020529 578 bp mRNA linear EST 03-DEC-2001
LOCUS sm4h02.y1 Gm-cl028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl028-6796 5' similar to SW:IAIC.SOYBN P31531
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ; mRNA sequence.

ACCESSION BE020529
VERSION BE020529.1 GI:8282968
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 578)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
A., Bolle,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)

TITLE Public Soybean EST Project
JOURNAL Contact: Shoemaker R/Public Soybean EST Project
COMMENT Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 3902 Std Error: 0.00
High quality sequence stop: 390.

FEATURES
source
1..578
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-6796"
/clone_lib="Gm-cl028"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; The mRNA was isolated from roots of Glycine max
'Supernod' plants generously donated by Dr. Gary Stacey.
The seedlings were inoculated with Bradyrhizobium
japonicus, strain USDA110 prior to harvest. StrataGene's
cDNA synthesis kit (catalog number 200401) was used to
synthesize the cDNA. First-strand synthesis was performed

with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGACAGAGAGACAGACTGCTGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After the second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL life technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Corvelli."

BASE COUNT	178 a	115 c	136 g	149 t
ORIGIN				

Query Match	25.3%	Score 486.8;	DB 9;	Length 578;
Best Local Similarity	90.1%	Pred. No. 8.5e-111;		

Matches 521; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy	236	aaatgggtcttgagaaatcagacttacctctgatttgggtgaagattggatactgaaca	295
Dδ	1	AAATGGGTCTTGC TGAGAATCAGCTACTTCTGATTGGTTGAAGATTGGATACTGAATA	60

Qy

296 accctgaagcctccatttgactccagaaggaaataatgatttcaggggccatagctaact 355
||||| || |

Dδ

61 ACCCAGAGGCTCCATTGCACACCAGAAGGAATAATGATTTCAGGGGCCATAGTAAC 120
||||| || |

QY 356 ttcaggattatcatgggtctggccgagttcagaaaatgctgtgctaaattatgctagaa 415
|||||
Db 121 TTCAGGATATCATGGGTCTGCCCGAGTTCAGAAATGCTGTGGCTAAATCATGGTAGAA 180
|||||

[illegible]

Qy 476 gagcacgaagtcaactgccttttggcagatcccggcaggcattcttadtgcca 535
|||||
Db 241 GAGCACGAAGTCACTACCTTTTGGTGGCAGACCTGGTGACGCATTTTGTGTGCCCA 300
|||||

Qy 536 ttccctattatccaggctttgaccgggatlttgaggtggagaacaggaggttaaacttgttc 595
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TTCCCTTATTATCCAGGTTTGTACCGSGATTTTGAGGTGGAGACAGGAATTAAACTGTTC 360

Qy 596 cagttatgtcgatagctcaaaataatttcgttgacaaaggaagcattggaagatgcct 655
|||||
Db 361 CAGTTATGTCGGATAGCTCAAAACAAATTTCAGTTGACAAAGCAAGCAATTGGACATGCGCT 420
|||||

Qy 656 atgagaagcaagagaggataacatcagagttaaaggtttactgatcaccaaatccatcaa 715
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dh 421 ATCAGAGACGCCAAACACACCATATATTATAAGCTAACAACCGCCGTCGTCTCATCAACCATAACCAATCAA 480

Qy 716 atccattaggcacaatcatggacagaagaagacactgagaacccgtgggtgagcttcacatg 775

OY 776 agaaagctatccaccttgtagtggatggaatatatgcT 813
||||| - | - ||||| |||||
DH 543 acgaccgtcgcaggcgagtcgcaaacgcatgacgat 570
||| | | | | | | | | |

RESULT 3
69450570

LOCUS	AM458572	536 bp	mRNA	linear	EST 03-DEC-2001
DEFINITION	sh10h02.y1 Gm-cl016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl016-4396.5' similar to SW:1A1C.SOYBN P31531				
	1'-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ; mRNA sequence.				

ACCESSION	AW458572
VERSION	AW458572.1
KEYWORDS	GI:7038789
EST.	EST.
SOURCE	soybean.

ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

REFERENCE
AUTHORS
1 (bases 1 to 536)
Shoenaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvelli, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, D., and Kane, J.

TITLE Public Soybean EST Project

Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Email: estewartson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1062 Std Error: 0.00

Insert Length: 1062 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 427.
Location/Qualifiers
source
1 536

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/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl016-4398"
/clone_lib="Gm-cl016"

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/tissue_type="immature flowers of field grown plants"
/lab_host="XL10-Gold"
/notes="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants."

```

from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly

(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the

pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Expelting."

	BASE COUNT	ORIGIN
	147 a	105 c
	134 g	149 t
	1 others	

Query Match 23.4%; Score 450.4; DB 9; Length 536;
Best Local Similarity 91.0%; Pred. No. 1e-101;
Matches 478; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

[illegible]

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QY 1125 ttctactggggggttgcccaagttggccataaagtcgttgccaaagcaatgctggtctatt 1184
|||||
Db 128 TTTCACTTCGGGGTTGGCCAAAGTTGGCATAAAGTCTTGCAAAGCAATAGCTGGTCTCTT 187

QY 1185 tctgtggatgatttaaggcaactctcctcaaaagccaaactttcgactctgaacaggact 1244
|||||
Db 188 TGTGTGGATGGATTTAAGCAACTTCTCAAGAAAGCCAAAGCTTGACTCTGAAATGGAGCT 247

QY 1245 ttggaaaagttaattcattcatgaagttaagatcaatgtttcacctggctattcccttcattg 1304
|||||
Db 248 TTGGAGAGTGATCAATCATGAGGTTAAGATCAATGTTTCACCTGGCTCTCTTCCATTG 307

QY 1305 cactgaagccagggttggttaggggtgctatgccaaactggatgatgctggtgctgcaaat 1364
|||||
Db 308 CACTGAGCCAGGGTGGTTTAGGGTGTGCTATGCCAACATGGATGATATGGCTGTGCAAA 367

QY 1365 tgccttgcaacgaatccgcaacttctgcttcaaaacaggagggtcggtgtctaaataa 1424
|||||
Db 368 TGCATTGCAAAAGATTCGAACCTTCGTGCTTCAAAACAGGAGGTCATGGTTCCTTAACAA 427

QY 1425 gaaacattgttggcagtaacttgaggtgagctcctcaaaacaggaaggttttgatgat 1484
|||||
Db 428 GAAACATTGCTGSCACAGTAATCTGAGGTTGAGCCTCANNACCAGAGGTTTGATGATAT 487

QY 1485 caccatgtcaactcaactcctccctcaactcagtcacactatggttaa 1529
|||
Db 488 CATGATGTCACTCACTCCCTATATACCTCAGTCCGCTTGGTTAAA 532

RESULT 4
BF649567 651 bp mRNA linear EST 20-DEC-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1. 651
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF079G12EC"
/tissue_type="Elicited cell culture"
/dev_stages="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/notes="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
```

```
BASE COUNT 207 a 83 c 147 g 210 t 4 others
ORIGIN

Query Match 20.6%; Score 396.2; DB 10; Length 651;
Best Local Similarity 77.7%; Pred. No. 3.7e-88;
Matches 505; Conservative 0; Mismatches 136; Indels 9; Gaps 2;

QY 853 gagatattagaggtgaacacagacatagagtgcagccgaacctcgttacacattgtttat 912
|||||
Db 1 GAATATATAGACATGACACACACATTTGAATGTGACCGTTAACTCGTTCACATAGTTTAC 60

QY 913 agctcttcaaaagacatggggtccctggcttcagagtcggcatcatatactcttacaat 972
|||||
Db 61 AGTCTTTCAAAAGACATGGGATTCCTGGTTTTAGAGTTGGTATAATATACTCTTATAAT 120

QY 973 gatgctggtttaaattgtgcagcaaaaatgtcaagctttgggattgggtgtcaacacagact 1032
|||||
Db 121 GATACCGTTGTAATTTGTGCACGAAATAATGTCAAGTTTGGATTTAGTTTCAACACACAGACA 180

QY 1033 cagtatcttttaagcatcgcgatgctaaatgatgatgtttgttgagaggtttctgpcagag 1092
|||||
Db 181 CAATACTTGTATGCGCAAAATGCTGCTGATGACGAGTTCGTTAAAAAGTTTCTTACTGAA 240

QY 1093 agtgcacaagaggttggttcgaagggttcaggttttcaactgggggttgccaaagtgtgc 1152
|||||
Db 241 AGTGCAAAAGAGGTTAGCACAAAGGTACAGAAATTTTCCACGATGGATTAAACCAAGTTGGA 300

QY 1153 ataaagtcttgcacaagaatcgtggtctattgtgtgagatttaaggaactcttc 1212
|||||
Db 301 ATTAATTTGTTTACAAGTAACCGTGGACATTTTGTGTGGATGGATTAGAGAGACTTCTT 360

QY 1213 aaaaagccaaactttgactcttgaacggagctttgaaagtattcattcatcaagttaag 1272
|||||
Db 361 AAGGAAGCTACATTTGAATCAGAAATTTGGAACATATGAGAGATGATATTTCACGAAGTTAAG 420

QY 1273 atcaatgtttccacctggcttccctccatcctgcactgagccgggtggttgggtgtgc 1332
|||||
Db 421 ATTAATGTTTCACTGGTGGTCTTTTTCATTTGTTGAGCCAGGGTGGTTTGAAGTGTGT 480

QY 1333 tatgccaacatgatgatgctgtgcaaatgtcttgcacaacgaatccgcaactttgtg 1392
|||||
Db 481 FATGCTAACATCGATGATAGACATGTGCCAAATTCGTTTACAAGGATTAAGTCATTGTGTG 540

QY 1393 cttc---aaaaaaggaggtcgtggtgtcctaataag-----aaacattgttggcacat 1443
|||||
Db 541 GTTCAGAATAAATGAAGAGGTTATGTTGCTCTGANAANAACACTAAACCTTGTGGCATACT 600

QY 1444 aacttgaggtcagcctcaaaaccaggaaggtttgatgatcaccatgtc 1493
|||||
Db 601 AATTTGAGGTTAAGCCTTAAACAAAGANGTTTGATGATATATTGTAATGTC 650

RESULT 5
BI974504 507 bp mRNA linear EST 30-NOV-2001
LOCUS
DEFINITION
ID: Gm-c1068-4001 5', similar to SW:1A1C.SOVBN P31531
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 507)
REFERENCE
AUTHORS
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
,Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
```


TITLE
JOURNAL
COMMENT

J.R., Ritter E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cu@resgen.com
High quality sequence stop: 357.

```

FEATURES
    source
        1. .507
            Location/Qualifiers
                db_xref="taxon:3847"
                /organism="Glycine max"
                /clone_lib="Gm-cl068"
                /clone_id="Gm-cl068-4001"
                /tissue_type="Leaf, drought stressed, 1 month old plants
                greenhouse grown"
                /lab_host="DH10B"
                /note="vector: pBluescript II SK+; Site.1: EcoRI; Site.2:
                XhoI; The cDNA library was constructed from mRNA isolated
                from drought stressed leaf tissue of the cultivar Willard
                82. The month old greenhouse grown plants were deprived
                water for 3 days prior to harvesting the stressed leaf
                tissue. Complementary DNA was synthesized from mRNA using
                a primer consisting of a poly(dT) sequence with a XhoI
                restriction site. EcoRI adapters were ligated to the
                blunt-ended cDNA fragments followed by XhoI digestion. The
                cDNA fragments were directionally cloned into the
                EcoRI-XhoI restriction site of the pBluescript vector. T
                ligated cDNA fragments were transformed into DH10B host
                cells (GibcoBRL). This library was constructed in the
                laboratory of Dr. Randy Shoemaker."
            134 a 102 c 107 g 164 t
               IGIN
                USE COUNT

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USE COUNT      134 a   102 c   107 g   164 t
IGIN
Query Match      20.28; Score 388.6; DB 10; Length 507;
Best Local Similarity 86.08; Pred. No. 2.8e-86;
Matches 446; Conservative 0; Mismatches 59; Indels 2; Gaps
1180 ctatttgtgtgatttaaggccaactctcaaaaagccaacttctcgactctgaacg 1239
      1 CTCCTTGTGTGGATTTAAGGCACACATCTCAAGAGCAACGCTTGACTCTGAATG 60
1240 gagctttggaagtattcatctcatgaagttaagatcaatgttccacctgctattcctc 1299
      61 GAGCTTTGGAGAGTGATCATTCATGAGTTTAAGATCAATGTTTCACCTGGCTCTCTTTC 120
1300 cattgcactgagccagggtgttaggggtgtgtctatgccaaacatgagatgagctgtg 1359
      121 CATTCGACTGAGCCAGGGTGGTTTAGGGTGTGCTTATGCCAACATGGATGATATGGCTGTG 180
1360 caaatgtctttgcaacgaatccgcaacttctgtgcttcaaaacagaggtcggtggtct 1419
      181 CAATGTGATGCTGCTTTTTTTCGAACCTCTGTGCTTCAAAACAGGAGGTGATGGTTCC 240
1420 aataagaacaattgttgccacagtaaacattgaggctgagcctcaaaacagagaagttgat 1479
      241 AACAGANAACATTGCTGGCAGTAACATTGAGGTTGAGCCTCAAAACCAAGGTTTGAT 300
1480 gatatcaacatgctcacctcacctctccoctcacctcagtcacctatggttaagccacaaa 1539
      301 GATATCATGATGTCACCTCACTCCCTTATACCTCAGTCCCTTTGGTTAAAGCCACAATT 360
1540 tgaagttgcattactctctgaatcgtt-ttaagaagaagtaactgatatactgaagattact 1598
      361 TGAGTTGGCAATATTTCTCGACCACTCTCAGAAGAAGTAACATGATATACGATGATATTT 420

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1599	ggttcttttattgttattttgagaaggtacataaagtgctgga-tttgtcttttgaaca	1657
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Db 121 AGAAGCATATGAAATGCACAAAAATCAAAACATCAAAAGTAAAGGTTGATTTTGACCAA 180

Qy 708 tccatcaaatccattagcgacaacatcatggacagaagacactgagaacccgtgtgagctt 767

Db 181 TCCATCAATCATTTGGGACCACATTTGGACAAACACACACTGAAGAAGTGCTTGAGTTT 240

Qy 768 catcaatgagaagcgtatccaccttgtatgtgatgaatatatgtgtgcaaacgttttcag 827

Db 241 CACCAACCAACAACATCCACCTTGTGTCGCAAAATCTACGCAGCCACTGTCTTTGA 300

Qy 828 caaacccgggttcataaagcatagctgagatatagaggatgaaacagacatagatgtga 887

Db 301 CAGCGCTCAATTCGTCAGTATAGCTCAAAATCCTCGATCAACAGSAAATGACTTACTGCAA 360

Qy 888 ccgcacccctcgacacattgtttatagctcttcacaaagacatggggttccctggctcag 947

Db 361 CAAGATTTAGTTCACATCGCTACAGCTTTCAAAAGACATGGGGTTACAGAGATTAG 420

Qy 948 agtcggcatcatatactctcaatgatgctgtgtggttaattgtgcacgcacaaatctcaag 1007

Db 421 AGTCGGAATCATATATTTCTTTTACGACGATGCTGTTAATTGTCTAGAAAAATGTCGAG 480

Qy 1008 ctttgattgggtcaacacgaactcgtatcttttttagcatcgatgctctaaatgatga 1067

Db 481 TTTTCGGTTAGTATCTACACAACCAATATTTTTTACGGCAATGCTATCGGACGAAAA 540

Qy 1068 gtttggagaggttcttggcagagatgcaaaagaggttggctcaaaaggttcagggtttt 1127

Db 541 ATTCTCGATATTTTCTTAAGAGAAAGCGGATGAGTTAGTAAAGGCACAAACATTT 600

Qy 1128 cactgggggggtggcgaagttggcataaaagtgtgtgcaaaagcaatgctgtctattgt 1187

Db 601 TACTAATGGACTTGAAGTAGTGGGAATTAATGCTTGAATAATATGCGGGCTTTTGTG 660

Qy 1188 ggggattgggttaaggcaactctcaaaaagcgaacttcga-ctctgaaacggagcctt 1246

Db 661 TTGGATGATTTTGGCTGCACATTTTAAAGGAATCGACTTTCGATAGCGAATGTCGGTAT 720

Qy 1247 ggaaggttatcatcatgaagtaagatcaatgtttccacctggctattcctt 1298

Db 721 GGAGAAGTATTATAACGATGTTAAGCTTAAGCTTCGCTCGCTTGGATCTTCGTT 772

RESULT 7

AW560294/c 623 bp mRNA linear EST 07-SEP-2000

LOCUS EST315342 DSIR Medicago truncatula cDNA clone pDSIR-26N23, mRNA

DEFINITION sequence.

ACCESSION AW560294

VERSION AW560294.1 GI:7205720

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 623)

AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.

TITLE ESTs from roots of Medicago truncatula after inoculation with Phytophthora medicaginis

JOURNAL Unpublished (1999)

COMMENT Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M251649e ; TIGR sequence name:MTBAW84TK ; More information, including clone ordering, is available at. .

'http://chryslie.tamu.edu/medicago'

Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

FEATURES

source 1..623

/organism="Medicago truncatula"

/cultivar="genotype Al7"

/db_xref="taxon:3880"

/clone="pDSIR-26N23"

/clone.lib="DSIR"

/tisue_type="roots infected with Phytophthora medicaginis"

/dev_stage="roots harvested at 10 days post inoculation with Phytophthora medicaginis"

/lab_host="E. coli strain XL0LR"

/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XL0LR cells. Note: EST may be of fungal origin."

BASE COUNT 205 a 138 c 83 g 197 t

ORIGIN

Query Match 18.3%; Score 351.8; DB 9; Length 623;

Best Local Similarity 77.1%; Pred. No. 4.5e-77;

Matches 457; Conservative 0; Mismatches 127; Indels 9; Gaps 2;

Qy 962 actcttacaatgatgctgtggttaattgtgcacgcacaaatgtcgaagctttggtggtgt 1021

Db 623 ACTCTTATATGATACCGGTGTAAATTTGTCAGCAAAATGTCAGTTTGGATTAGTTT 564

Qy 1022 caacacagactcagtatcttttagcatcgatctaataatgatgatgtttgtggagagt 1081

Db 563 CAACACAGACACATACTTGTATGGCGCAAAATGCTGCTGATGACGAGTTCGTTAAAAAGT 504

Qy 1082 ttctggcagagatgcaaaaggttggctcaaaagttcagggttttccactgggggttgg 1141

Db 503 TTTTCTACTGAAAGTGCAAGAGGTTAGCACAAAGGTACAGAAATTTTCACAGTGGATTAA 444

Qy 1142 ccaaaagttggcataaagtctgtgcaaaagcaatgctggtctattgtgtggatggatttaa 1201

Db 443 CCAAAAGTTGGAATTAATCTTTTACAAAGTACGGTGGACTTTTGTGTGATGGATTGA 384

Qy 1202 ggcacacttcacaaagccaaacttgcactctgaaacggagctttggaaagtatacttc 1261

Db 383 GAGGACTTTTAAAGGAAGCTACATTTGMAATCAGAAATTTGGAACCTATGGAGAGTATTTC 324

Qy 1262 atgaagttaaagatcaatgtttcacctggctattcctccactgactgacagccaggtgtg 1321

Db 323 ACCAAGTTAAGATTAAATGTTTCCACCTGGTGTCTTTTCATTGTTCTGAGCAGGGTGTG 264

Qy 1322 tttaggtgtgctatgccaaacatggatgatgctgtgcaaatgtcttggcaacgaaatcc 1381

Db 263 TTAGAGTGTGTTATGCTACATCGATGATAGAGATGTGCAAATTCGTTTACAAAGGATTA 204

Qy 1382 gcaactttgtgcttc---aaaacaaaggaggtcgtgtgctcctaataag-----aaacatt 1432

Db 203 GGTCAATTTGTGCTCAGATAATAAGGAGGTTATGCTGTCTGAGAAAGACACATAAACCTT 144

Qy 1433 gttgcacagtaacttgaggctgagcctcaaaacacagaaggtttgatgatcaccatgt 1492

Db 143 GTTGGCATAGTAATTTTGAGCTTAAGCCTTTAAACAAGAAAGGTTTGATGATATATGTAATGT 84

Qy 1493 caccctcactctcccctacccctcagtcacctatggtttaaaagccacaaatgagtt 1545

Db 83 CACCTCATTTCTCCATTTCTCCTCAGTCACCTCTTGTGTTAAAGCCCACTACTTGAATT 31

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RESULT 8
BM095045
LOCUS BM095045 479 bp mRNA linear EST 30-NOV-2001
DEFINITION saj25f06.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl066-3732 5' similar to SW:1A1C_SOYBN P31531
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.
ACCESSION BM095045
VERSION 1 GI:17024011
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 479)
AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpellding, J., Corvelli, V., Khanna
, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
FEATURES
Location/Qualifiers
1..479
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl066-3732"
/clone_lib="Gm-cl066"
/tissue_type="Leaf and shoot tip, salt stressed, 2 week
old seedling"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."
BASE COUNT 128 a 92 c 104 g 155 t
ORIGIN
Query Match 18.1%; Score 349; DB 10; Length 479;
Best Local Similarity 88.3%; Pred. No. 2.1e-76;
Matches 391; Conservative 0; Mismatches 50; Indels 2; Gaps 1;
QY 1247 ggaagtattcatcgaagttaagaatcaattttccaccctgctattccctcattgca 1306
DB 1 GGAGAGTGATCATGTGAGGTGAAGATCAATGTTTCACTGCTGCTCTTTCCATTGCA 60
QY 1307 ctgagccagggtgttaggtgtgctatgcccaacatgatatgctgtgcaattg 1366
|||||

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Db 61 CTGAGCCAGCGTGGTTTGGGTGTGCTATGCCAACATGGATGATATGCTGTGCAAAATTG 120
QY 1367 ctttgcaacgaatccgcacaaatttgcctcaaaaagaaggaggtcgtggtgctctaataaga 1426
|||||
Db 121 CATTTGCAAGAATTCGTAACCTTTGTGCTTCAAAAAGAGGATCATGCTGCTTAACAAGA 180
QY 1427 aacattgtggcacagtaacttgaggctgagcctcaaaacaccagaaggtttgatgatca 1486
|||||
Db 181 AACATTGTTGGCACAGTAACCTTGAGGTTTGAGCCCTCAAAACACAGAAAGTTTGAATATATCA 240
QY 1487 ccatgtcacctcactctcccctacctcagtcacctatggttaaaagccacaaaattgagttt 1546
|||||
Db 241 TGATGTCACTCACTCCCCCATACCTCAGTCACCTCTGGTTAAAGCCACAAATTTGAGTTG 300
QY 1547 gcatattccctcgaatcggttagaagaagtaactgatgatggaagattacttggtctttt 1606
|||||
Db 301 GCATATTCTCTGAACCCCTAGAGAAGTAACATGATATATGATGATTATTGGCTCTCTT 360
QY 1607 tattgttatttgagaaggtacataaa--gtgctggattgttcttcttgggaacagcaataa 1664
|||||
Db 361 GACTTGTGTTGTTGGCAAGGTACATAAAGTCTTGAGTCTTGTATTATTAAACAGCAGTAA 420
QY 1665 caggaaattcctgatgtgtttt 1687
|||||
Db 421 CAGGCAATGCTGATATGTTTT 443
RESULT 9
BF650933
LOCUS BF650933 630 bp mRNA linear EST 20-DEC-2000
DEFINITION NF102B08ECF1047 Elicited cell culture Medicago truncatula cDNA
ACCESSION BF650933
VERSION BF650933.1 GI:11916063
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 630)
AUTHORS Torres-Jerez, I., Scott, A. D., Harris, A. R., Gonzales, R. A., Bell, C. J.,
Flores, H. R., Iman, J. T., Weller, J. W. and May, G. D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
Center for Medicago Genomics Research
JOURNAL Unpublished (2000)
COMMENT Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 630 Std Error: 0.00
Plate: 102 row: B column: 06
Seq primer: TCACACGGAACACGCTATGAC.
FEATURES
Location/Qualifiers
1..630
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_lib="NF102B08EC"
/tissue_type="Elicited cell culture"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/notes="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
BASE COUNT 186 a 115 c 121 g 205 t
ORIGIN

```


BF648314
LOCUS
DEFINITION BP648314 653 bp mRNA linear EST 20-DEC-2000
clone NF046D07EC 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 653)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Iman, J.F., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
Center for Medicago Genomics Research
Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 653 Std Error: 0.00
Plate: 046 row: D column: 07
Seq primer: TCACACGAGGAACAGCTATGAC.
Location/Qualifiers
1. .653
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_lib="NF046D07EC"
/tissue_type="Elicited cell culture"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
BASE COUNT 194 a 123 c 118 g 216 t 2 others
ORIGIN
Query Match 17.4%; Score 334.8; DB 10; Length 653;
Best Local Similarity 82.3%; Pred. No. 8.1e-73;
Matches 395; Conservative 0; Mismatches 84; Indels 1; Gaps 1;
QY 88 atgggtttcaaggccatggaccacactcccttgggtccaagatggctattggggatgga 147
DB 174 ATGGGACTTGTGAGCATGGACCAACCCCAATTTGTTCTCAAGATAGCCACTGGTGATGGA 233
QY 148 catggcgaatccccactattgtgatggaagcttatcatcaaaacccctttcat 207
DB 234 CARGGTGAACATCATCTTACTTTGATGGATGAAGACCTTATGATAAAACCCCTTTTCAT 293
QY 208 ccacagataatcctaaccgtgttatgcaaatgggtctgtgagaaatcagcttacctct 267
DB 294 CCAACCAAAATCCTCAAGGTGTATCCAAATGGGTCTTCAGAGATACAGTTACTTGCT 353
QY 268 gatttggtgaagattggatgactgaacaaacccctgaagccctccattcattcagcagaagga 327
DB 354 GATTGGTTCAAAATTTGGATAATGAGTAAACCCAGAACCTCAATTTGCTACTAGAAAGGA 413
QY 328 ataaatgatttcaggccatagctaaacttcaggattatcatggtctggccgagttcaga 387
DB 414 GTACACAAATTTCAAGAAATTTGGCTAATTTTCAGGATTTATCATGCTTACAGAGTTTCA 473
QY 388 aatgctgtggctaaattatggctagacaaggggaaacagaatcacgtttgacctgac 447
|||||

Db 474 AATGCTGTGGCTAAATTCATGCTCAAGAACAGAGAAATAGAGTGACATTTGATCCTGAT 533
QY 448 cgtattgtcatgagcgggtggagccacggagcacacgaagtcactgctttgtttggca 507
|||||
Db 534 CGTATTGTCATGAGTGGTGGAGCAACTGGAGCATGANGCACTGCTTTTGTGGCA 593
QY 508 gatccggcagcattcttagtgcctattccc-tattatccaggcttgaccgggattt 566
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Db 594 GATCCTGGTGATGCTTTTGGTGGCTACACCTTACTATNCAGGATTTGATCGAGATTT 653
RESULT 12
LOCUS
DEFINITION AI898099 672 bp mRNA linear EST 18-MAY-2001
EST267542 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLED31P17, mRNA sequence.
ACCESSION AI898099
VERSION AI898099.1 GI:5604001
KEYWORDS EST.
SOURCE tomato.
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 672)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman,
C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley,
S.D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.
Location/Qualifiers
1. .672
/organism="Lycopersicon esculentum"
/cultivar="TA96"
/db_xref="taxon:4081"
/clone="CLED31P17"
/clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF"
/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLED - Tomato carpel EST Library. OligodT-primed and
directionally cloned cDNA in vector Lambda ZAP II with 5',
and 3' ends located at the EcoRI and XhoI sites,
respectively."
BASE COUNT 228 a 102 c 139 g 202 t 1 others
ORIGIN
Query Match 16.8%; Score 323.4; DB 9; Length 672;
Best Local Similarity 68.9%; Pred. No. 5.7e-70;
Matches 460; Conservative 0; Mismatches 202; Indels 6; Gaps 1;
QY 436 tttagacctgacctattgtcatgagcgggtggagccacggagcacacgaagtcactgccc 495
DB 10 TTTGATCCAAAGAAATAGTATGATGGAGGAGCAACAGGAGCTCATGAANGTTGGCA 69
QY 496 ttgtttgtcagatcccgccgagcattcttagtgcctattccattatccaggttt 555
DB 70 TTTTGTGGCTGATCTCTGGTGATGTCATTTCTTCTTACACCATATTTATCCAGGATTT 129
QY 556 gaccgggatttgagtggtggagaacaggagttaaacttgttccagttatgtgcatagctcca 615
DB 130 GATAGAGATTGAGATCGAGATCGAGAGAGTACAACTTTTCTCTGTTGTTGTGAGAGTTCT 189
|||||

QY 616 ataattttgttgcacaaagaagcattggaagatgcttatgagaagaagagagat 675
Db 190 AACAAATTCAGGTAACAAAGACGCTTAGAAGAGCATAGTAAAGCTCAAGATCA 249
QY 676 aacatcaagtaaaaggtttactatcaccaatccatccatccattaggaacacatg 735
Db 250 AATATCAAGTAAAGGATTACTTATAACCAATCCATCAATCCATAGGTACAAATTTG 309
QY 736 gacagaagacactgagaacqgtggtgagcttcacatgagaagcgctatccaccttga 795
Db 310 GACAGGAACATTAAGACATATTAAGATTCATCAATGACAAAACATACATCTAGTA 369
QY 796 tctgtgaaatatactgcgaacagtttttcagccacccggttttcataagcattag 855
Db 370 TGTGATGAATCTATGCAACACCGGTTTAGTCAACCTTCATTCATCAGTATCTCAGAA 429
QY 856 atattagaggatgaacagacatagagttgaccgcaacctcgtacacattgttatagt 915
Db 430 GTCAAGAGTCA-----ACTTGTGGATGCAACGATGATTTAGTACACATTTGTATAGT 483
QY 916 ctttcaagagacatgggttccctggtctcagagtcggtcattacatactcttacaatgat 975
Db 484 CTATCGAAGATCTAGGGTTCTCGATTAGGTTGGATTATTTACTCGTACATGAT 543
QY 976 gctgtggttaattgtgcacgcaaaatgcaagctttgagttggtgtcaacacagactcag 1035
Db 544 GCGGTGTCAATATTCAGCATAGATGCAAGTTTGGACTTTGGACTTTGTTCAACACAAACACAA 603
QY 1036 tatcttttagcattcatgtaaatgatgatgagtttggagaggtttcttgcagagagt 1095
Db 604 AGATTGATTGCTCAATGTTATTAGACACTATCTTTGNTGNTGAAGATTTCATCCGGAAGAC 663
QY 1096 gcaaaagag 1103
Db 664 TCGATGAG 671

RESULT 13
BE555018
LOCUS BE555018 468 bp mRNA linear EST 04-DEC-2001
DEFINITION spB3q02.v1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl045-267 5' similar to SW:1A1C_SOYBN P31531
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.
ACCESSION BE555018
VERSION BE555018.1 GI:9819505
KEYWORDS soybean.
SOURCE Glycine max
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 468)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Harro,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Willson,R.
Public Soybean EST Project
Unpublished (1999)
CONTACT: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 913 Std Error: 0.00
High quality sequence stop: 434.

FEATURES
source Location/Qualifiers
1..468
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-267"
/clone_lib="Gm-cl045"
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
/note="Vector: pBluescriptII SK+; Site.1: EcoRI; Site.2:
XhoI; This cDNA library was constructed from mRNA isolated
from etiolated hypocotyl tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) primer with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by digestion with EcoRI and XhoI. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(Gibco BRL). This library was constructed by Dr. Randy
Shoemaker."
BASE COUNT 137 a 93 c 98 g 140 t
ORIGIN
Query Match 16.8%; Score 322.4; DB 10; Length 468;
Best Local Similarity 89.5%; Pred. No. 9.3e-70;
Matches 358; Conservative 0; Mismatches 41; Indels 1; Gaps 1;
QY 1217 agccaaatttcgactctgaacggagcttggaagattatcattcgaagtgatca 1276
Db 4 AGCCAAACGGTTGACTCTGAATGGAGCTTTGGAGAGTGATTCATGAGGTTAAGATCA 63
QY 1277 atgtttcacctgctattcctccattgcactgagccagggtgttaggtgtgctga 1336
Db 64 ATGTTTCACCTGCCTCTTCTTCCATTTGCACAGCCAGGGTGGTTTAGGGTGTGCTATG 123
QY 1337 ccaacatggatgatggctgtgcaaaattgcttgcacgaatccgcaactttgtgcttc 1396
Db 124 CCACATGATGATATGGCTGTGCAAAATTCATTTGCAAGAAATTCGAACCTTCGTCTTC 183
QY 1397 aaaaacaggagctgctgtgtctataaagaacattgttggcacagtaacttgagctga 1456
Db 184 AAAACAAGGAGGTCATGGTTCTCTAACAGAAACATTTGCTGGCAGACGTAATCTGAGTTGA 243
QY 1457 gctcaaaaccagaggtttgatgatcaccatgctcactctccctaccctcagt 1516
Db 244 GCCTCAAAACCAAGAGTTTGATGATATCATGATGTCACCTCACCTATACCTCAGT 303
QY 1517 caccatgtgttaagccacaaattgagtttgcatattcctctgaatcgt-ttagaagaag 1575
Db 304 CCCCTTTGGTTAAAGCCACAATTTGAGTTGCCATATTTCTCTGCACCATCTCAGAGAAG 363
QY 1576 taactgatgtgaagattacttggtttctttattttgtta 1615
Db 364 TAACGTATATACGATGATTTATTTGGTCTTTGATTGTTTA 403

RESULT 14
LOCUS AI484859 575 bp mRNA linear EST 18-MAY-2001
DEFINITION EST243120 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLED2N19, mRNA sequence.
ACCESSION AI484859
VERSION AI484859.1 GI:4380230
KEYWORDS EST.
SOURCE Tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 575)

www.pearsoned.com/uk

respectively.

```

100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES             Location/Qualifiers
     source            1..819
                        /organism="Lycopersicon esculentum"
                        /cultivar="TA96"
                        /db_xref="taxon:4081"
                        /clone="cLEC68H15"
                        /clone_lib="tomato callus, TAMU"
                        /tissue_type="callus"
                        /dev_stage="25-40 days old"
                        /lab_host="XLI-Blue MRF."
                        /note="Vector: pBlueScript SK(-); Site.1: EcoRI; Site.2:
                        XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons
                        of seedlings 7-10 days post-germination were excised, cut
                        at both ends and placed on MS medium with no selection.
                        Mixed callus was harvested at 25 and 40 days and included
                        undifferentiated masses. tomato Callus EST Library"
BASE COUNT           259 a      133 c      177 g      250 t
ORIGIN
Query Match          16.4%; Score 316.2; DB 10; Length 819;
Best Local Similarity 63.5%; Pred. No. 3.8e-68;
Matches 521; Conservative 0; Mismatches 288; Indels 12; Gaps 2;

QY  697  ctgatcaccatccataatccattaggcacaatcatgatgcagaagaacactagaacc 756
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   1  CTTTAAACAACACCTTCAAAATCCATTAGTACTCTTCTTCAAGAGACACACTCCGTCGAC 60

QY  757  gtggtgagcttcacatgagaagcgtatccacctgtatgtatgataaatatgtctgca 816
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   61  ATTGTAAGTTTCATCAACTCGAAAACATCCATTAGTATGCGATGAATCTATGCTGCT 120

QY  817  acagttttcagccaaccgggtttcataagcatagctgagattatagaggatgaacagac 876
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   121  ACGGTGTTTGATCAGCCTAGATTTCATCAGTGTATCTGAAATAGTTGAGGAT-----ATG 174

QY  877  atagagtgtgaccgcaacctcgtaacacatgttttatagttctcaaggacatggggttc 936
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   175  ATTGAATGCACAAGAAGATTTGATCCATATAGCTATAGCTTGCTTAAAGACTTGGGATTT 234

QY  937  cctggcttcagatcggcatacatctctacaatgctgtggttaattgccaagc 996
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DB   235  CCAGATTCAAGTTGGAAATGTTTACTCGTACACCATACGATAGTAAACATTGCTTAGA 294

QY  997  aaatgtcaagcttggattgggtgtcaacacagactcagtatcttttagcatcgatgcta 1056
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```



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Db 295 AAGATGTCAGGCTTTGGGTAGTTCAACTCAGACACACACATTTGCTTGCAATCAATGTTG 354
QY 1057 aatgatgatgagtttctgtgagaggttctctggcagagagtgcaaaaggttggtgctcaaagg 1116
Db 355 TCTGATGAAGTATTCTATTCACAAAATTCATTGCTGAGAGTTCCGAAAGACTCGGAGAAAGG 414
QY 1117 ttcaaggggttttcaacttgggggggttggccaaagtgtgcaaaagtgccttgcaaaagcaatgct 1176
Db 415 CAGGGGATGTTTACAAAAGGACTAGCAGAAGTTGGAATTAGTACATTTGAAAAGCAATGCT 474
QY 1177 ggtctatttctgtgagatttaaggcaactctcctcaaaaagccaaactttcgactctgaa 1236
Db 475 GGTGTTGTTTCTGGATGGAATTAAGGAGGCTCTTAAGAGAGCAACATTTGATAGTGAG 534
QY 1237 acggagctttggaagtttatcatcatgaagttaagatcaaatgtttcacctgggtctatcc 1296
Db 535 TTAGAATTATGCGAGAATTATTATCAATCAATGAAGTGAACCTTAATGTGTTTCACAGGATGTTCA 594
QY 1297 ttccattgcactgagccagggttggtttaggggtgtgctatgccaacatggatgatggt 1356
Db 595 TTTTCATTGTTCTGAACCTCGTTGGTTTAGAGTTTGTGTTTGTGCAAAACATGGATGACGAGACG 654
QY 1357 gtgcaaatgctttgcacgaatccgcaactttgtgcttcaaaacaagg-----aggtc 1410
Db 655 ATGAGGATGCAATTAAGAAGGATAAGTTACTTTGTGCTTACCCAAAGGACTTAACAC 714
QY 1411 gtgtgtcttaataagaacattgttggcacagtaacttgaggctgagcctcaaaaccaga 1470
Db 715 ATTGCTGCTATTAAAGAAACAATGCAGAGGAGGAAACTTCAGATCAGCTTATCGTTTCGA 774
QY 1471 aggtttgatgatatacccatgtcacctcaactctccctacc 1511
Db 775 AGATGGGATCATGAGTTTCATGAACCTACCAGCTCACTCTCC 815
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Search completed: August 21, 2002, 00:26:04
Job time: 5655 sec

Db 1561 ATCGTTTAGAAGAGTAAGTATGATGTAAGATTACCTTGGTCTTTTATTTTATTTTATTTT 1620
 Qy 1621 agaaggtacataagtgctgatttcttcttcttcttcttcttcttcttcttcttcttcttctg 1680
 Db 1621 AGAAGGTACATAAGTGTGCTGATTTGTTCTTTGGAACCAATACAGAAATTCCTGATG 1680
 Qy 1681 ttgtttgtatcgccatcccaatccagtgctcctacaagttgtgtcttcttcttcttcttctc 1740
 Db 1681 TTGTTTGTGATCGGCATACATCCAGTGCTCTACAAGTTGTCTGCTCTCATGCGCC 1740
 Qy 1741 cctcaatcttaggggcatcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1800
 Db 1741 CTTTCAATCTTAGGGCATTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1800
 Qy 1801 ttatagagctgaatgtatgtattgtttatcagagagtcacaaagatcttcttcttcttctg 1860
 Db 1801 TTTATAGAGTCTGTAATGTATTGTTTATCAGAAAGAGTCCAAAGAGTGTCTGTAATCTG 1860
 Qy 1861 ctactgaattgttaacttcaattatgaataaattgttaataaaggcttcttcaaatcttct 1920
 Db 1861 CTACTGAATGTAACTTCAATATGAATAAATTTGTAATAAGGCTTCAAAATTCATT 1920
 Qy 1921 tcc 1923
 Db 1921 TCC 1923

RESULT 2:

GMCACCS1
 LOCUS G.max mRNA for ACC synthase. 1789 bp mRNA linear PLN 11-MAY-1995
 DEFINITION G.max mRNA for ACC synthase.
 ACCESSION X67100
 VERSION X67100.1 GI:18557
 KEYWORDS ACC synthase.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1. (bases 1 to 1789)
 Direct Submission
 TITLE Submitted (29-JUN-1992) N. Li, USDA/ARS Plant Mol Biol Lab, B-006
 JOURNAL BARC West, Beltsville MD 20705, USA
 2. (bases 1 to 1789)
 Liu, D., Li, N. and Mattoo, A.K.
 Nucleotide sequence of soybean ACC synthase
 JOURNAL Unpublished
 FEATURES
 source 1..1789
 /organism="Glycine max"
 /cultivar="century"
 /db_xref="taxon:3847"
 /tissue_type="leaf"
 /dev_stage="mature plant"
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 /product="1-aminocyclopropane 1-carboxylate synthase"
 /protein_id="CAA47474.1"
 /db_xref="GI:18558"
 /translation="MGLMDVDQTLKSMVIGDHGEASPYFDGWKAYDENPFPKFN
 PNGVIQMLAENLTSDLVEDWILNNPEASICTPEGINDFRAINFQDYHGLPEFRNA
 VAKFMGRNRYTFDPDRIVMSGGATGAHEVTFCLADPCDAFLVPYPYGFDRDL
 RWTGKLVPMCDSSNNPKLTQALEDAVEKAKEDNIRVKGLLITNPSNPLVTMDR
 NTLRTVMSFINEKRIHIVSDEIYSATVFSHPHSFISAEILBEDTDECRLNLIHYS
 LSKDMGPPGRGVITISYDVAHVCAKMSFGLVSTQYTOYLKASMLNDEFVESFLV
 ESARKDGRHRVTGLKYGKICLQSNAGLFLVMDLRLQLKKPTDLSEMLNDEFVRIID
 EVKINYPSSGSEFTCEPWFRCVYANNDDMAVQIALQRIIRNFVQLNKEINVPNKKHCW
 HSNRLSLKTRRFDLIMSPHSPIPOSPLVKAT"

BASE COUNT

532 a

338 c

402 g

517 t

ORIGIN

Query Match 70.9%; Score 1363.8; DB 8; Length 1789;
 Best Local Similarity 90.8%; Pred. No. 0;
 Matches 1464; Conservative 0; Mismatches 147; Indels 2; Gaps 1;
 Qy 77 acatacaccatattggtttcaagccatggaccacaaactcccccttgttcccaagatggcta 136
 Db 152 ACATAGACTATATGGGTTGATGATGTGGACCAACATCAATTTGTTGCTAAGATGGTCA 211
 Qy 137 ttggggatggacatggggaatcattcccccatcttcttgatggatgaaggtcttatgatcaaa 196
 Db 212 TCGGAGATGGACATGGTGAACCATCACCATACTTTGATGGATGAAGGCTTATGATGAA 271
 Qy 197 acccttctatccacacagataatcctcaacggtgttatgcaaatgggtcttctctgagaatc 256
 Db 272 ACCCTTTTCATCCCAAGAGAAATCCTAACGGGTTATCCAAATGGTCTTCTGCTGAGAATC 331
 Qy 257 agcttacctgtattggttgaagattggatactgaacacacccctgaagctccatttgca 316
 Db 332 AGCTTACTTCTGATTTGGTTGAAGATTGGATACCTGAATAACCCAGAGGCCCTCCATTTCGA 391
 Qy 317 ctccagaaggaataaattgatttcaggccatagctaaactttcaggattatcatgtctgg 376
 Db 392 CACCAGAAGGAATAAATGATTTTCAGGCCATAGCTAACTTTTCAGGATTTATCATGGTCTGC 451
 Qy 377 ccgagttcagaaatgctgtgctgctaaatttatggctagaacaaaggggaaacagaatcacgt 436
 Db 452 CCGAGTTTCAGAAATGCTGTGGCTAAATTCATGGGTAGAACAAAGAGGAAACAGAGTCACGT 511
 Qy 437 ttgacctgacctgattgtctgagcgtgagcgtgagccacacggagacacagacagtcagct 496
 Db 512 TTGATCCTGACCGTATTGTCTATGAGCGGTGGAGCAACTGGAGACACACCAAGTCATACCT 571
 Qy 497 ttgttggcagatcccgccgagcgatcttcttagtgccattccctattatccaggtcttg 556
 Db 572 TTTGTTGGCAGACCCCTGGTGACGCATTTTGGTGGCCATTTCCCTATTATTCACAGGTTTG 631
 Qy 557 accgggatttgagtgagacacagggagttaaacttgttccagttatgtgcagatagctcaa 616
 Db 632 ACCGGGATTTGAGGTGGAGAAACAGGAATTAACCTTTGTTCCAGTTATGTGCGATAGCTCAA 691
 Qy 617 ataatttctgtttacaaaaggaacattggaagatgcctatgaaagacagagagagata 676
 Db 692 ACAATTTCAAGTTGACAAAGCAAGCATTTGGAAGATGCGTATGAGAAGCCCAAGAGGATA 751
 Qy 677 acatcagagtaaggggttactgatcaccaatccatccatccatccatccatccatccatccat 736
 Db 752 ATATAAGAGTAAGGGCTTGCTCATCACCANTCCATCAACCCATTAGGCACAGTCATGG 811
 Qy 737 acagaagacactgagaaacggtgtgagcttctcaaatgagaagcgtatccaccttctgtat 796
 Db 812 ACAGAAACACACTAAGAACCCGTGATGAGCTTTCATCAACGAGAAGCGTATCCACCTTGAT 871
 Qy 797 gtgatgaataatagtctgcaacagtttccagccacacccgggttccataagcagtagtgaga 856
 Db 872 CTGATGAATATATCTCTGCAACAGTTTTTTAGCCCCCCCCAGTTTCTATAAGCATTTGCTGAGA 931
 Qy 857 tattagagatgaac 916
 Db 932 TATTAGAGGAAGACACACACACATCGATGTGACCGCAACCTCGTTCCACATTGTTTATATGC 991
 Qy 917 ttcaaaaggacatgggggttccctggctcagagtcgagtcgagtcgagtcgagtcgagtcgagtc 976
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VERSION AY062022.1 GI:17266327
KEYWORDS
SOURCE Medicago
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 1850)
AUTHORS Engstrom,E.M. and Long,S.R.
TITLE MtACC synthase, a putative 1-aminocyclopropanecarboxylic acid
synthase from Medicago truncatula
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1850)
AUTHORS Engstrom,E.M. and Long,S.R.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2001) Biological Sciences, Stanford University,
371 Serra Mall, Stanford, CA 94305-5020, USA
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AF016459
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Pisum sativum 1849 bp mRNA linear PLN 23-JUL-2001
AF016459.1 GI:2360988
SOURCE
pea.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.
1 (bases 1 to 1849)
Peck, S.C. and Kende, H.
A gene encoding 1-aminocyclopropane-1-carboxylate (ACC) synthase
produces two transcripts: elucidation of a conserved response
Plant J. 14 (5), 573-581 (1998)
MEDLINE
98340552
PUBMED
9675901
2 (bases 1 to 1849)
Peck, S.C. and Kende, H.
Differential regulation of genes encoding
1-aminocyclopropane-1-carboxylate (ACC) synthase in etiolated pea
seedlings: effects of indole-3-acetic acid, wounding, and ethylene
Plant Mol. Biol. 38 (6), 977-982 (1998)
9908479
REFERENCE
3 (bases 1 to 1849)

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AUTHORS

Peck, S.C. and Kende, H.

TITLE

Direct Submission

JOURNAL

Submitted (30-JUL-1997) MSU-DOE Plant Research Laboratory, Michigan State University, Plant Biology Building, East Lansing, MI 48824-1312, USA

FEATURES

source

Location/Qualifiers
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/dev_stage="seedlings"

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ORIGIN

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Matches 1206; Conservative 0; Mismatches 360; Indels 15; Gaps 4;

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Qy 268 gatttggtgaagattggtgatactgaacacccctgaagcctcattgcactccaagaaga 327

Db 318 GATATGGTTCAAAATGGATTTATGATTAATCCAGAAGCTTCGATTTGTACGTAGAAGA 377

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RESULT 7

LOCUS E12805 1864 bp DNA linear PAT 24-JUN-1998
DEFINITION cDNA encoding poplar ACC (1-aminocyclopropane-1-carbonic acid) synthetase which is induced by ozone.
ACCESSION E12805
VERSION E12805.1 GI:3251637
KEYWORDS JP 1997075088-A/1.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1864)
AUTHORS Hoya, I. and Kitani, S.
TITLE OZONE-DERIVED 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID-SYNTHESIZING ENZYME GENE GROUP OF WOODY PLANT
JOURNAL Patent: JP 1997075088-A 1 25-MAR-1997;
COMMENT OS Populus nigra L. (poplar)
PN JP 1997075088-A/1
PD 25-MAR-1997
PF 07-SEP-1995 JP 1995254510
PI HOYA IZUMI, KITANI SHIGEKAZU
PC C12N15/09,C07H21/04,C12N9/88//A01H5/00,(C12N9/88,C12R1:19); CC
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CC hypothetical: No;
CC anti-sense: No;

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FEATURES

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 QY 1487 ccattgacctcactctccctacacctcagtcacattgatttaaaagccacaatt 1540
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RESULT 9
 AB034993
 LOCUS
 DEFINITION Malus domestica MdACS-5B mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds.
 ACCESSION AB034993
 VERSION AB034993.1 GI:7209852
 KEYWORDS 1-aminocyclopropane-1-carboxylate synthase.
 SOURCE Malus domestica cDNA to mRNA.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 AUTHORS Sunako,T., Ishikawa,R., Senda,M., Akada,S., Niiizeki,M. and Harada,T.
 TITLE MdACS-5A (Accession No. AB034992) and 5B (Accession No. AB034993), two wound-responsive genes encoding 1-aminocyclopropane-1-carboxylate synthase in apple. (PGR00-030)
 JOURNAL Plant Physiol. 122, 620 (2000)
 REFERENCE 2 (bases 1 to 1838)
 AUTHORS Harada,T.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-1999) Takeo Harada, Hirosaki University, Faculty of Agriculture and Life Science, Bunkyocho 3, Hirosaki, Aomori 036-8561, Japan (E-mail:tharada@cc.hirosaki-u.ac.jp, Tel:81-172-39-3777, Fax:81-172-39-3750)

FEATURES
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 BASE COUNT 528 a 371 c 412 g 527 t
 ORIGIN

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Qy	1278	tgtttcaactggctattctctccattgcaactgagccagggtgtttaggggtgctatgc	1337
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Qy	1398	aaacaagaggtcggtggtctcataaag---aaacattgttggcacagtaacttgaggct	1454
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Qy	1455	gagcctcaaaaccagaaggtttgatgatgatcacatgtcacc	1496
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AF386523			
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DEFINITION		Pyrus communis 1-aminocyclopropane 1-carboxylate synthase 5 (ACGS5)	PLN 21-JAN-2002
ACCESSION		mRNA, complete cds.	
VERSION		AF386523.1	GI:18252346
KEYWORDS		pear.	
SOURCE		Pyrus communis	
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.	
REFERENCE		1 (bases 1 to 1770)	
AUTHORS		El Sharkawy, I., Li, Z.G., Latche, A. and Lelievre, J.M.	
TITLE		Ripening related genes in pear (Pyrus communis)	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 1770)	
AUTHORS		El Sharkawy, I., Li, Z.G., Latche, A. and Lelievre, J.M.	
TITLE		Direct Submission	
JOURNAL		Submitted (30-MAY-2001) Biologie Molculaire et Physiologie de la Maturation des Fruits, INP - ENSAT, Av. de l'Agrobiopole - BP107, Castanet Tolosan Cedex 31326, France.	
FEATURES		Location/Qualifiers	
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BASE COUNT	493 a	381 c	418 g	478 t
ORIGIN				

Query Match 40.5%; Score 778.6; DB 8; Length 1770;
Best Local Similarity 72.5%; Pred. No. 6.5e-190;
Matches 1051; Conservative 0; Mismatches 389; Indels 9;

3

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Qy	258	gcttaacct	gtatttggttgaag	ttagtact	gaacaa	cccttgaag	ctccatttgac	317								
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Db	642	CAGAG	ATTTGGG	TGGCGA	ACGGG	GTGC	AACTGAT	PAC	CAGTTCGCTGTGACAGCTCCAA 701							
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Db	1596	TACACCGAT	1604

RESULT 11

CSIO12551	CSIO12551	1734 bp	linear	PLN 26-JAN-2000
LOCUS	Citrus sinensis mRNA for ACC synthase.			
DEFINITION	AJ012551			
ACCESSION	AJ012551.1	GI:6433835		
VERSION	ACC synthase; ACS1 gene.			
KEYWORDS	Citrus sinensis.			
SOURCE	Citrus sinensis.			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.			
REFERENCE	Wong, W.S., Ning, W., Xu, P.L., Kung, S.D., Yang, S.F. and Li, N.			
AUTHORS	1 (bases 1 to 1734)			
TITLE	Identification of two chilling-regulated 1-aminocyclopropane-1-carboxylate synthase genes from citrus (Citrus sinensis Osbeck) fruit			
JOURNAL	Plant Mol. Biol. 41 (5), 587-600 (1999)			
MEDLINE	20108317			
REFERENCE	2 (bases 1 to 1734)			
AUTHORS	Wong, W.S.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-NOV-1998) Wong W.S., Biology, The Hong Kong University of Science and Technology, Rm.6207, Biology Department, HKUST, Clear Water Bay, Kowloon, HONG KONG			
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 BASE COUNT 479 a 349 c 393 g 513 t
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Query Match 40.3%; Score 775.2; DB 8; Length 1734;
 Best Local Similarity 72.3%; Pred. No. 4.9e-189;
 Matches 1066; Conservative 0; Mismatches 393; Indels 15; Gaps 4;

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RESULT 12
 CPU68216 1888 bp mRNA linear PLN 31-DEC-1998
 LOCUS Carica papaya ACC synthase mRNA, complete cds.
 DEFINITION U68216
 ACCESSION U68216
 VERSION U68216.1 GI:4090534
 KEYWORDS
 SOURCE papaya.
 ORGANISM Carica papaya
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Caricaceae; Carica.
 REFERENCE 1 (bases 1 to 1888)
 AUTHORS Neupane,K.R., Mukatira,U.T. and Stiles,J.I.
 TITLE Cloning of Fruit-Specific ACC Synthase and ACC Oxidase cDNAs From
 Papaya (Carica papaya L.) and Their Expression During Fruit
 Ripening
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1888)
 AUTHORS Neupane,K.R., Mukatira,U.T. and Stiles,J.I.
 TITLE Direct Submission
 JOURNAL Submitted (28-AUG-1996) Plant Molecular Physiology, College of
 Tropical Agriculture and Human Resources, University of Hawaii,
 3190 Malle Way, St John #503, Honolulu, HI 96822, USA
 FEATURES
 Location/Qualifiers
 source
 /organism="Carica papaya"

TITLE	Direct Submission
JOURNAL	Submitted (07-FEB-1997) Horticulture, Pennsylvania State University, 102 Tyson Building, University Park, PA 16802, USA
FEATURES	Location/Qualifiers
source	1. .1757 /organism="Pelargonium x hortorum" /strain="88-51-10" /db_xref="taxon:4031" /tissue_type="pistil" /dev_stage="receptive to pollination"
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CDS	89. .1558 /gene="GACS2" /note="similar to Pelargonium hortorum clone pGAC-2, Genbank Accession Number U17231" /codon_start=1 /product="1-aminocyclopropane-1-carboxylate synthase" /protein_id="AAB70885.1" /db_xref="GI:1877497" /translation="MYNMSSTTQRTLLSKMATGDGHGENSPYFDGWKAYDNNPFHIT QNFQVGMGLAQWLSFELIEQLVNLPPOASTCTAGLQEFKDTAIFODYHGLPEFR YAVANPMGVKGRNVTFNPDRIVNSGGATGAHEMIAFLADPGDAFLVPYPYGPDR DLWRCTQVLIPVCSENNPRTISRLEAYERAQEDNIRVGILLINPNPLGLIL DRETLSLVSAFKINEKHILVDCAEIIYAATFSQPAVSIAVEIQENVSCNRDLIHVI SLSDKMDFPFGRIYVSYNDVAVNCARMSSEGLSVSTQTQHLIASMLSDDEVFDTI VESAKRLAIRRYTTFTRGLAQVNTIGCLKSGNLGFLIMDLRLLKEKTFFEAEMALRWII NEVKLVNPSGAFTHCSEPGRFCFAMDDLTMOVALRRITITFALQNKEAAVLPAIKR QCQWNNGRLSLSFRRPDDFTFMSPSHSPIQSPLVRAT"
BASE COUNT	528 a 378 c 405 g 446 t
ORIGIN	
Query Match	37.4% Score 719.2; DB 8; Length 1757;
Best Local Similarity	70.9%; Pred. No. 1.3e-174;
Matches 1000; Conservative	0; Mismatches 398; Indels 12; Gaps 3;
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Qy	167 actttgatgtaggaaggcttatgatcaaaaacccttcattcccacagataaatcctaacy 226
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Qy	227 gtgttatgcaaatggcttgtctagaatcagcttaacctgtatttggtgaatatgga 286
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Qy	287 tactgaacaacccctgaagcctccattgcacttcagaaaggaataaaatgatttcagggcc 346
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Qy	407 tggetagaaaaaaggggaaaaagaatacacgttttgaccctgaacctgattgcatgagcggtg 466
Db	414 TGGGAAAGGTGAGAGGAAACAGAGATAACATTTAACCCAGATGCGCATATGTTATGAGTGGAG 473
Qy	467 gagccacggagcacagaagtcactgctttgttggcagatcccgcgagagcattct 526
Db	474 GAGCAACTGGAGACTCATGAAATGATTGCTTCTGTTTGGCTGTGATCCTGGCCGATGCTTTTC 533
Qy	527 tagtgccattccctattatccaggtcttgaccgggatttgagtggaagacagagtta 586
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Db	594 AGCTAAATTCCTGTAGTCTGTGAAAGTGAACAAATTTTCAGGATCATCCCAGTAGTGCCTTAG 653

REFERENCE	1 (bases 1 to 1868)
AUTHORS	Hoya, I. and Kitani, S.
TITLE	OZONE-DERIVED 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID-SYNTHESIZING
JOURNAL	ENZYME GENE GROUP OF WOODY PLANT
COMMENT	Patent: JP 1997075088-A 2 25-MAR-1997; TOYOTA MOTOR CORP OS Populus nigra L. (poplar) PN JP 1997075088-A/2 PD 25-MAR-1997 PF 07-SEP-1995 JP 1995254510 PI HOYA IZUMI, KITANI SHIGEKAZU PC C12N15/09, C07H21/04, C12N9/88//A01H5/00, (C12N9/88, C12R1.19); CC strandedness: Double; CC topology: Linear; CC hypothetical: No; CC anti-sense: No; FH Key Location/Qualifiers FT source 1..1868 FT /tissue_type='Leaf' /organism='Populus nigra L.' FT FT /clone='pPNA CCS2' FT 5'UTR 1..118 FT CDS 119..1579 FT /product='Poplar ACC (1-aminocyclopropane-1-carbonic acid) FT FT synthetase which is induced by ozone' FT 3'UTR 1580..1868. FEATURES Location/Qualifiers source 1..1868 /db_xref='taxon:32644' BASE COUNT 590 a 366 c 405 g 507 t ORIGIN Query Match 36.08; Score 691.6; DB 6; Length 1868; Best Local Similarity 71.79; Pred. No. 1.8e-167; Matches 923; Conservative 0; Mismatches 359; Indels 6; Gaps 1; Qy 119 tgttgcacagatgctcattggggatggacatgcgaatcccatcccatcattgatgat 178 Db 138 TTTTGTCCAGATTGCAACGATGATGACATGGAGAGAACTCCCATATTTTGTATGAT 197 Qy 179 ggaaggttatgatcaaaaccccttccatccacagataatcctaacggtgttatgcaaa 238 Db 198 GGAAGGCTTAGCATATAAACCCCTTTTCACTACTGACAAACCCCGATGGAGTATACAAA 257 Qy 239 tgggtcttctgagaatcagcttacctctcattggttggaagattggaatcgaacacc 298 Db 258 TGGGTCTAGCAGAAATACAGCTTTCCTGCTGATTGATGATGATGATGATGATGAT 317 Qy 299 ctgaagctccattgctcactccagaagaataatgatttccagggccatagctaaatttc 358 Db 318 CCAAGGCTCCATTGGCAATCCCTGAAGAGTTTATATGTTCAAGGATATTGCTTAACCTTC 377 Qy 359 agattatcatggtctggtccgagttcagaatgctgtggtcaaaatttatggctagaacaa 418 Db 378 AGGATTATATGCGCTGCCAGAGTTTCGACAGGCTATTGCGAAGTTTATGCGGAGAGTTA 437 Qy 419 ggggaaacagaatacagtttgaccctgacccgttatgttcattgagcggaccacggag 478 Db 438 GAGGAGGAAGGGTGACATTTTATGATCCAGATCCCATAGTATGATGATGATGATGAT 497 Qy 479 cacacgaagcactgctcgtttgttgccagatcccgagagcattcttagtgcctattc 538 Db 498 CAACGAGCTGATCATGTTTGGCTGGCCGATCCCGGGATGCTTTCCTTGTTCCTTC 557 Qy 539 cctattatccaggtcttgaccggatttgagggtggaacagaggttaaactgttccag 598 Db 558 CTTTACTATCTGCTATCTATCGAGACCTTGGATGGCGACTGGGGTCCAGATTGTTCCAG 617 Qy 599 ttatgctgatagctcaataatttctgcttgacaaaggagcatttgggaagatgcctatg 658

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Db	1392	TACACGATTTGTCGGTGAACAAAAGGA	1419
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AB033503			
LOCUS	1868 bp	mRNA	linear
DEFINITION	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds.		PLN 15-APR-2000
ACCESSION	AB033503		
VERSION	AB033503.1	GI:7576443	
KEYWORDS	1-aminocyclopropane-1-carboxylate synthase.		
SOURCE	Populus euramericana (cultivar:I-45/51) cDNA to mRNA.		
ORGANISM	Populus euramericana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.		
AUTHORS	Koch, J.R., Minocha, R., Nakajima, N., Yasutani, I., Saji, H., Rebeck, J. and Davis, K.R.		
TITLE	Induction of ethylene and putrescine by ozone: Comparison of an		

ozone-sensitive and an ozone-tolerant hybrid popular clone
Unpublished (1999)
2 (bases 1 to 1868)
Nakajima, N., Yasutani, I., Koch, J. R., Minocha, R., Saiji, H.,
Rebeck, J., and Davis, K. R.
Direct Submission
Submitted (12-OCT-1999) Nobuyoshi Nakajima, The National Institute
for Environmental Studies, Regional Environment Division; Onogawa
16-2, Tsukuba, Ibaraki 305-0053, Japan (E-mail: naka-320@nies.go.jp,
Tel: 81-298-50-2490, Fax: 81-298-50-2490)
Location/Qualifiers
1. 1868
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BASE COUNT 590 a 366 c 405 g 507 t
ORIGIN
Query Match 36.0%; Score 691.6; DB 8; Length 1868;
Best Local Similarity 71.7%; Pred. No. 1.8e-167;
Matches 923; Conservative 0; Mismatches 359; Indels 6; Gaps 1;
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Db 438 GAGGAGGAAGGTCACATTTGATCCAGATCCCATAGTATGAGCGGTGGAGCAACTGGAG 497
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2002, 00:26:40 ; Search time 58.79 Seconds
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914.436 Million cell updates/sec

Title: US-09-763-957-2

Perfect score: 2559

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2559	100.0	484	21	AA179292 Mung bean 1-aminocyclopropane-1-carboxylic acid synthase.
2	1881.5	73.5	484	18	AAW21754 Poplar 1-aminocyclopropane-1-carboxylic acid synthase.
3	1875.5	73.3	490	19	AAW60235 Pelargonium 1-aminocyclopropane-1-carboxylic acid synthase.
4	1823	71.2	487	19	AAW57484 Papaya ACC synthase.
5	1771.5	69.2	483	22	AAE00986 Tomato 1-aminocyclopropane-1-carboxylic acid synthase.
6	1771.5	69.2	483	22	AAE59724 Tomato ACC synthase.
7	1765	69.0	504	19	AAW52818 Coffee-fruit spec
8	1762.5	68.9	483	12	AAW15509 Tomato ACC synthase.
9	1762.5	68.9	486	18	AAW21755 Poplar 1-aminocyclopropane-1-carboxylic acid synthase.
10	1755.5	68.6	485	22	AAE00985 Tomato 1-aminocyclopropane-1-carboxylic acid synthase.
11	1755.5	68.6	485	22	AAE59723 Tomato ACC synthase.

12	1746.5	68.2	485	12	AAE15508 Tomato ACC synthase
13	1713	66.9	485	12	AAE15507 Tomato ACC synthase
14	1713	66.9	485	19	AAW47314 Tomato 1-aminocyclopropane-1-carboxylic acid synthase
15	1713	66.9	485	22	AAE00984 Protein encoded by
16	1713	66.9	485	22	AAE59720 Tomato ACC synthase
17	1713	66.9	485	22	AAE59725 Tomato ACC synthase
18	1710	66.8	485	12	AAE15506 Tomato ACC synthase
19	1710	66.8	485	19	AAW47313 Tomato ACC synthase
20	1710	66.8	485	22	AAE00983 Tomato 1-aminocyclopropane-1-carboxylic acid synthase
21	1710	66.8	485	22	AAE59719 Tomato ACC synthase
22	1702.5	66.5	482	19	AAW60233 Pelargonium 1-aminocyclopropane-1-carboxylic acid synthase
23	1698.5	66.4	482	19	AAW60234 ACC synthase
24	1696	66.3	485	19	AAW39422 ACC synthase
25	1676.5	65.5	482	18	AAW09878 ACC synthase
26	1637.5	64.0	390	18	AAW09879 ACC synthase
27	1637.5	64.0	493	12	AAE15504 Zucchini ACC synthase
28	1637.5	64.0	493	19	AAW47310 Protein encoded by
29	1637.5	64.0	493	22	AAE00980 Zucchini 1-aminocyclopropane-1-carboxylic acid synthase
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31	1636.5	64.0	493	12	AAE15505 Zucchini ACC synthase
32	1636.5	64.0	493	19	AAW47311 Zucchini ACC synthase
33	1636.5	64.0	493	22	AAE00981 Zucchini 1-aminocyclopropane-1-carboxylic acid synthase
34	1636.5	64.0	493	22	AAE59717 Protein encoded by
35	1636.5	64.0	493	22	AAE59721 Zucchini ACC synthase
36	1633.5	63.8	493	13	AAE25406 ACC synthase
37	1627.5	63.6	494	12	AAE15863 Zucchini ACC synthase
38	1627.5	63.6	494	19	AAW47312 Zucchini ACC synthase
39	1627.5	63.6	494	22	AAE00982 Zucchini 1-aminocyclopropane-1-carboxylic acid synthase
40	1627.5	63.6	494	22	AAE59718 Protein encoded by
41	1627.5	63.6	494	22	AAE59722 Zucchini ACC synthase
42	1603.5	62.7	517	17	AAW04558 Carnation ACC synthase
43	1573	61.5	496	15	AAE53114 Crucifer 1-aminocyclopropane-1-carboxylic acid synthase
44	1563	61.1	476	22	AAE00988 Tomato 1-aminocyclopropane-1-carboxylic acid synthase
45	1563	61.1	476	22	AAE59727 Tomato ACC synthase

ALIGNMENTS

RESULT 1

AA179292

ID AA179292 standard; Protein; 484 AA.

XX AA179292;

XX 03-JUL-2000 (first entry)

DT Mung bean 1-aminocyclopropane-1-carboxylic acid synthase.

DE Mung bean; 1-aminocyclopropane-1-carboxylic acid synthase;

XX ACC synthase; AIM-1; promoter; pGEL-1; transgenic plant.

OS Vigna radiata.

XX WO200012714-A1.

XX 09-MAR-2000.

XX 31-AUG-1999; 99WO-AU00705.

XX 31-AUG-1998; 98AU-0005572.

XX (UYQU) UNIV QUEENSLAND.

XX Botella Mesa JR, Cazzonelli CI;

XX WPI; 2000-270821/23.

XX N-PSDB; AA294267.

Isolated nucleic acid molecule for producing transgenic plants having altered characteristics such as resistance to a plant pathogen comprises promoter, inducible in response to physical stimulation -

PS Claim 4iv; Page 101-103; lllpp; English.

XX The present sequence is that of 1-aminocyclopropane-1-carboxylic acid synthase (ACC synthase) of mung bean. ACC synthase expression is induced in response to mechanical strain, auxin and salt stress. CC is induced in response to mechanical strain, auxin and salt stress. CC The invention relates to the promoter, pGEL-1 (see AA294266), of the ACC synthase gene, AIM-1. pGEL-1 is capable of induction by CC physical and/or environmental stimuli in cells in which it is CC indigenous and, in the absence of any negative regulatory mechanism, CC is capable of constitutive expression in cells in which it is CC non-indigenous. The promoter can be used to direct expression of CC genes conferring useful traits on plants, such as improved CC resistance to a plant pathogen, altered nutritional characteristics, CC expression of a plantabody, altered biochemical pathway, altered CC fertility, and/or altered flower colour.

XX Sequence 484 AA;

SQ

Query Match 100.0%; Score 2559; DB 21; Length 484;

Best Local Similarity 100.0%; Pred. No. 1.6e-247;

Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFKAMDQTPLLSKAIGDHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTS 60

DB 1 mgykamdqtpllskmaigdhgesspyfdgwkydqpnhphtdnpngvmqglanqlts 60

QY 61 DLVEDWILNPPASICTPGINDFRAIANFODYHGLAEFRNAVAKFMARTGRNRTFDPD 120

DB 61 dlvedwilnppasictpgindfraianfodyhglaefrnavakfmartgrnrtfdpd 120

QY 121 RIVMSGGATGAHEVTAFCIADGAEFLVPIPYPGFDRDLRWRGTGKLVPMVDCSSNNFV 180

DB 121 rivmsggatgahvtafciaadgaeaflvpipypgfdrdlrwtgklypvmcdssnnfv 180

QY 181 LTKEALEDAYEKAREDNIRVKGILLTNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDIEI 240

DB 181 ltkealedayekarednirvkgilltnpsnplgtimdrktrlrtvvsfinekrihlvcdiei 240

QY 241 YAATVFSQPGFTISAEIIDEDETDIECDRLNHLVHVSLSKDMGFPGRVGIYISYNDVAVN 300

DB 241 yaatvfsqpgftisaeiideadediecdrlnhlvhvselskdmgfpgrvgiysyndavvn 300

QY 301 CARKMSSFGVSTQTYQLASMLNDEFEVERFLAESAKRLAQRFVFTGGLAKVGKICLQ 360

DB 301 carkmssfgvstqtyqlasmlndefeverflaesakrlaqrfvftgglakvgkiclq 360

QY 361 SNAGLFVWMDLRLQLKKPTFSETELWKVIIHEVKINVSFGSFHCTEPGFRVCYANMD 420

DB 361 snaglfvwmldrlqlkkptfsetelwkvihevkinvsgsfhctepgfrvcyanmd 420

QY 421 DMAVQIALQIRNFVLQNKVVVSNKKHCWHSNLRSLKTRFDDITMSPHSPPLQSPMV 480

DB 421 dnavqialqirnfvlqnkvvsnkkhchwshnlrslktrfdditmsphspplqspmv 480

QY 481 KATN 484

DB 481 katn 484

RESULT 2

AAW21754

ID AAW21754 standard; Protein; 481 AA.

XX

AC AAW21754;

XX

XX 26-AUG-1997 (first entry)

DE Poplar 1-aminocyclopropane-1-carboxylic acid synthase PNACCS1.

XX

XX Ozone; induction; exposure; resistance; transgenic plant; ACC1;

KW 1-aminocyclopropane-1-carboxylic acid biosynthesis.

XX

OS Poplar nigra.

XX

PN JP09075088-A.

XX

PD 25-MAR-1997.

XX

XX 07-SEP-1995; 95JP-0254510.

PF

XX 07-SEP-1995; 95JP-0254510.

PR

XX (TOYT) TOYOTA JIDOSHA KK.

PA

XX WPI; 1997-239270/22.

DR

XX N-PSDB; AAT73501.

XX

PT Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic

PT enzyme genes - from poplar tree, are useful for generating

PT ozone-resistant trees and pollution clean-up trees

XX

PS Claim 2; Pages 7-9; 12pp; Japanese.

XX

CC This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase

CC encoded by a cDNA clone isolated from poplar trees which

CC had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone

CC for 6 hours after one hour acclimation at 25 degrees C, 70 % relative

CC humidity, 30 k lux and air current 30 cm/second. The gene will be

CC useful for breeding air pollutant ozone-resistant trees, especially

CC poplar.

XX

SQ Sequence 481 AA;

Query Match 73.5%; Score 1881.5; DB 18; Length 481;

Best Local Similarity 73.5%; Pred. No. 1.3e-179;

Matches 349; Conservative 58; Mismatches 65; Indels 3; Gaps 2;

QY 11 LLSKMAIGDHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTSLDVEDWILNN 70

DB 9 lllrlassgdhgedspfdgwkydqpnhphtdnpngvlgmglanqlcfdldlqdwllkn 68

QY 71 PRASICTPGINDFRAIANFODYHGLAEFRNAVAKFMARTGRNRTFDPDRIVMSGGATG 130

DB 69 phasicspeglnefrfelaifgdyhgipefrnavanmekvrgnrvtfcdpdrivmsggatg 128

QY 131 AHEVTAFCIADGAEFLVPIPYPGFDRDLRWRGTGKLVPMVDCSSNNFVLTKAEALDAY 190

DB 129 ahetiafciaadgaeaflvpipypgfdrdlrwtgklypvdssannfmvtrealenay 188

QY 191 EKAREDNIRVKGILLTNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDIEIYAATVFSQPG 250

DB 189 ekaqldnkvkgilltnpsnplgtildretlrsivfineknhlvcdelyaatvfsqpd 248

QY 251 FTSIAEILEDDETDIECDRLNHLVHVSLSKDMGFPGRVGIYISYNDVAVNCARKMSSFGL 310

DB 249 flsvrrillge--dlcndlvhivyslskdmgfpgrlvvgliysyndavvscarkmssfgl 306

QY 311 VSTQTYQLASMLNDEFEVERFLAESAKRLAQRFVFTGGLAKVGKICLQ-SNAGLFVWM 369

DB 307 vstqtyqlasmlsdnefemfieskrilaaryvftgldvgieclksnagflwm 366

QY 370 DLRLQLKKPTFSETELWKVIIHEVKINVSFGSFHCTEPGFRVCYANMDMAVQIALQ 429

DB 367 dslrllkqtkfaemalwrvihevklinvspgcsfclxpgwfrvcfanmdetmqvals 426

QY 430 RIRNFVLQNKVVVSNKKHCWHSNLRSLKTRFDDITMSPHSPPLQSPMVKATN 484

DB 427 riktfnvkeadtkskrnlrwqgslklusprlyddfinshpspibpqsplvrarn 481

RESULT 3

AAW60235

ID AAW60235 standard; Protein; 490 AA.

XX

AAW60235;
 28-SEP-1998 (first entry)
 Pelargonium 1-aminocyclopropane-1-carboxylase synthase.
 ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
 ethylene; transgenic plant; wilting; geranium; pphsacc49.
 Pelargonium x hortorum cv. Sincerity.
 WO9814465-A1.
 09-APR-1998.
 30-SEP-1997; 97WO-US17644.
 01-OCT-1996; 96US-0724194.
 (COLS) UNIV COLORADO STATE RES FOUND.
 Ranu RS;
 WPI; 1998-260994/23.
 N-PSDB; AAV30326.
 New isolated ACC synthase genes - are obtained from geranium and
 rose, used to develop products for producing plants with reduced
 ethylene levels, for increasing shelf-life
 Claim 58; Fig 8; 77pp; English.
 This amino acid sequence of this 1-aminocyclopropane-1-carboxylate
 synthase (ACC synthase) of geranium cv. Sincerity was deduced from
 isolated cDNA clone pHSacc49 (see AAV30326). This ACC synthase has a
 mol.wt. of 55.1 kDa and is designated as a Group II enzyme; 2
 Group I geranium ACC synthases (see AAW60233 and AAW60234) are also
 claimed. The invention relates to new isolated ACC synthase genes
 from geranium and rose (see AAV30324-26 and AAV30330) and the use of
 antisense fragments of these genes to control expression of ACC
 synthase genes in transgenic plants, especially in geranium, rose
 and woody plants. By reducing the amount of ACC synthase produced
 in plant cells, the rate of ACC conversion to ethylene can be
 decreased. This can be used to prolong the shelf-life of cut
 flowers and to reduce leaf yellowing and petal abscission during
 shipping and storage.
 Sequence 490 AA;
 Query Match 73.3%; Score 1875.5; DB 19; Length 490;
 Best Local Similarity 71.9%; Pred. No. 5.3e-179;
 Matches 348; Conservative 68; Mismatches 59; Indels 9; Gaps 6;
 QY 7 DQPLLSKMAIGDGHGSSPYFGWKAYDONPHPTDNPNGVMGLAENQLTSDLYEDW 66
 DB 9 nqrtlslskmatgghngenspyfgwkaydnphfhtcnpqgvgiqmglaenqlsllelqgw 68
 QY 67 ILANPEASICTPEGINDFRAIANFDYHGLAEFRNAVAKENARTGRNRTFDPDRIVMSG 126
 DB 69 vlnnpqasictagglqefktaifqdyhglqssdmfianfmkgvgrnrvfnpdrivmsg 128
 QY 127 GATGAHEVTAFCADPGAEALVPIYPYGGFDRDLRWRTGKLVLP-VMCDSSNNEFLVKEA 185
 DB 129 gatgahemiafcladpgdafivtpypygfdrlrwtgvtgvlipvvvcesennfrlrsa 188
 QY 186 LEDAYEKAREDNIRVKGLLTITNPSNPGLTMDRTLTVTVSFNEKRIHLVCDIYAATV 245
 DB 189 ledayeraqedkrlrvkgllitnpsnplgtaldretivslvsvfneknihlvcdieiyatv 248
 QY 246 FSQPGFTISAEILLEDEIDICEDRLNHLVITYSLSKDMGFPFGFRVGIITYSYNDVAVNCARM 305
 DB 249 fsqapfvslaevieqe-nvscnrldlhivyslskdmgfpfgfrvgyisyndavvncarm 307

QY 306 SSFGLVSTQYQYLLASMLNDDVEVERFLASAKRLAQRFRVFTGGLAKVGIKIQSNAGL 365
 DB 308 ssfglvstqyqyghliasmldsdvdfvtfivesakrlaryttftrglagvngiclsnggl 367
 QY 366 FVMDLRQLLKPTFDSETELWKVIIIEVKINVSFGYSFHCTEPGWFRCVYANMDDNAVO 425
 DB 368 fvmldlrllikekfcaemalwrvinvekvlnvsgasfchcsepgwfrvcfanmddltmq 427
 QY 426 IALQRIENFVLONKEVVV--SNKKHCWHSNL-RLSLKTRRFDIT---MSPHSLPQSPM 479
 DB 428 valriitfalqnkeavlpalkrcqwgqnnlgrlslsfrifddftmspmshpsl-qsp1 486
 QY 480 VKAT 483
 DB 487 vrat 490
 RESULT 4
 AAW57484
 .ID AAW57484 standard; Protein; 487 AA.
 XX
 AC AAW57484;
 DT 13-AUG-1998 (first entry)
 XX
 DE Papaya ACC synthase enzyme.
 KW Papaya; ACC synthase; ethylene biosynthesis; fruit ripening; enzyme;
 KW 1-aminocyclopropane-1-carboxylic acid synthase; regulation.
 OS Carica papaya.
 XX
 PN US5767376-A.
 PD 16-JUN-1998.
 XX
 PF 07-JUN-1995; 95US-0485107.
 PR 07-JUN-1995; 95US-0485107.
 PA (UYHA-) UNIV HAWAII.
 XX
 PI Neupane KR, Stiles JI;
 XX
 DR WPI; 1998-361822/31.
 DR N-PSDB; AAV31482.
 XX
 PT Papaya ACC synthase cDNA sequence - useful for regulating ethylene
 biosynthesis in the ripening of fruit
 PS Claim 7; Columns 35-40; 33pp; English.
 XX
 CC This is a papaya 1-aminocyclopropane-1-carboxylic acid synthase (ACC
 synthase). The encoding nucleotide sequences are useful for the
 recombinant production and control of ACC synthase in transformed plants
 and cells, especially to control fruit ripening. The enzyme converts
 s-adenosylmethionine to ACC in the biosynthesis of ethylene, which is
 responsible for the ripening of fruit (ACC is converted to ethylene by
 ACC oxidase). Commercial tropical fruit markets e.g. papaya production,
 require fruits in an adequately ripened state. Ripening is dependent on
 various conditions such as temperature and time. By providing ACC
 synthase coding sequences, the endogenous enzyme can be inhibited using
 antisense constructs, until it reaches its destination, then allowed to
 ripen, or be used in recombinant cells which can produce ethylene and in
 turn ripen fruit. Control or inhibition of ethylene production with
 nucleic acids is safer than chemical means, which can be toxic, and
 cannot be used for commercial inhibition.
 XX
 SQ Sequence 487 AA;

Query Match 71.2%; Score 1823; DB 19; Length 487;

Best Local Similarity 70.9%; pred. No. 9.7e-174; Matches 339; Conservative 65; Mismatches 66; Indels 8; Gaps 3

Qy 11 LLSKMAIGDGHGESSPYEDGKWKADQNPHTDPNGVQMGLAENQLTSDLVEDWILNN 70
||||| : ||||| ||||| : ||||| ||||| ||||| ||||| : ||||| ||||| : |||||
Db 10 llskiatanghgedspydqwkaydsdpfhtqpegvilqmglaengcfnlihewlkn 69
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 71 PEASICTPEGINDFRAINFQDYHGLAEFRNAVAKFMARTGNRITFDPPDRIVMSGGATG 130
Db 70 peasictaaggaefrdiaifqdyhglaefreavakfmgkvrnrasfdpdrivmsggatg 129
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 131 AHEVTAFCIADPGCAFLPIPIYPYQDFDRDLRWRTGKVLVPVCMDSNNFVLTKEALEDAY 190
Db 130 aheviafciadpgdaflvptpyyqgfdrlrtwrtgkvlpvvccssndyqitialeaay 189
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 191 EKAREDNTRVGLLTINPSNPLGTTIMDKTKLRTVVVSFINEKRIHLVCDIYAAVFSQPG 250
Db 190 etageadikvkgllipnpsnplgtitkdtlealvtfnhknhlvcdeiyaatvfsqpe 249
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 251 FISTAIEILEDTECDRLNHLVHYLSLKGDMGFCGFRVGIIVSYNDVAVNCARKMSSFCL 310
Db 250 ftsiaieile-edkiccnrdlhlhlyslkgdmgffgfrvgyisyndavvscarkmssfgl 308
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 311 VSTQTYLLASMLNDDFERVERPLAESAKRLAQRFVFTGGLAKVGIKCLQSNAGLFVWMD 370
Db 309 vssqtqyliasmldedfvqgfivesrkrkrlamrhaftqrlaqvginciksnagifvwmd 368
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 371 LROLLKKPTDSETELKWKVILHEVKINYPGYSFHCTEPGFRVCYANWMDMAVOIALQR 430
Db 369 lrrllkedtfeamvlwrvilnelkinyvspgssfhcsepgfrvvcfanmddktmeialsr 428
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 431 IRNFVLQNKVYVSNKKHCWHSNRLSLKTRRFDIT-----MSPHSPLPQSPMWKA 482
Db 429 iktfmlqkheamvpkkkicwqtsrlsfss-ryedimetpgsfmshpapiqspvlvra 485
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 5
AAE00986 ID AAE00986 standard; Protein; 483 AA.
XX AC AAE00986;
XX DT 04-JUL-2001 (first entry)
XX DE Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC 1B.
XX KW Tomato; 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC 1B;
XX KW ethylene production; fruit ripening; transgenic plant.
XX OS Lycopersicon esculentum.
XX PN QS6207881-B1.
XX PD 27-MAR-2001.
XX PF 25-JAN-1995; 95US-0378313.
XX PR 19-APR-1992; 92US-0862493.
XX PR 10-SEP-1990; 90US-0579896.
XX PA (USDA) US SEC OF AGRIC.
XX PI Theologis A, Sato T;
XX DR WPT; 2001-289591/30.
XX Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic
XX acid synthase, LE-ACC2 useful for producing ACC synthase which is
XX essential for the production of ethylene in higher plants -
XX Example 3; Fig 10; 92pp; English.
XX The present sequence is tomato 1-aminocyclopropane-1-carboxylic acid

XX PA (USDA) US DEPT OF AGRICULTURE.
 XX PI Sato T, Theologis A;
 XX KW WPI; 2001-079558/09.
 XX OS
 XX XX Expression cassette for producing transgenic plants exhibiting
 PT inhibited ethylene production and delayed fruit ripening, comprises
 PT complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic acid
 PT synthase synthesis -
 XX XX
 XX Example 3; Fig 10; 91pp; English.
 XX PS
 XX CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for
 CC the production of ethylene in higher plants; ethylene is a determinant
 CC of fruit ripening. The present invention relates to an expression
 CC cassette which comprises the reverse transcript of RNA complementary to
 CC an RNA transcribed from ACC synthase gene. The expression cassette can be
 CC used to prevent ACC gene expression. The expression cassette is useful
 CC for inhibiting ethylene production and fruit ripening, when introduced
 CC into a plant or plant cells. The present sequence is the protein encoded
 CC by tomato ACC synthase gene LE-ACC1B(b) clone. This sequence was used in
 CC a sequence homology comparison with other ACC synthase gene clones
 CC (AAB59721-B59727).
 XX XX
 XX SQ Sequence 483 AA;
 XX
 Query Match 69.2%; Score 1771.5; DB 22; Length 483;
 Best Local Similarity 68.9%; Pred. No. 1.4e-168;
 Matches 326; Conservative 76; Mismatches 66; Indels 5; Gaps 3;
 QY 11 LLSKMAIGDGHGESSPYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTSDLVEDWTLNN 70
 Db 13 llskmatndghenspyfdgkayannpfltdnptvgmglaenqlctdlleewmnn 72
 QY 71 PEASICTPEGINDFRAITANFDYHGLAEFRNAVAKFMARTGRNRTFDPDRIVMSGATG 130
 Db 73 pkasictvegaenfqdlafqdyhgypcfrqavarmekvrgdrvtfdpnrvmsgatg 132
 QY 131 AHEVTAFLADPGEAFVLPIYPYPGFDRDLWRRTGKVLVPMCDSSNNFNLTKEALRDAY 190
 Db 133 ahemlafcladpgeafvlptpypgfdrlwrtgvlfpvcescndfkvtkaaleay 192
 QY 191 EKAREDNIRVKGLLITNPNPLGTIMDRKTLRTVVSFINKRIHLVCEIYAATVFSQPG 250
 Db 193 ekaqgsnikikgllinnpsnplgtltdktlrdvtfinsknihlvceiyaatvfdqpr 252
 QY 251 FISTAEITLEDTECDRLNVHIVYSLSKDMGPPGFRVGIYISYNDVAVNCARKMSSFGL 310
 Db 253 fivsvemveem--lecnldihivyslskdglfpgrvgyvgyndvtvnlsrkmsfgl 310
 QY 311 VSTQTYLLASMLNDDEVERFLAESAKRLAQRFVRFTGGIAKVGIKLQSNAGLFWMD 370
 Db 311 vstqtqhmiasmdelifevkefaesserlgkqgmftkglagvgistlksnaglfvmd 370
 QY 371 LRQLLKPTFDESELMKVYIIEVKINVSFGYFHCTEPGWFRVCYANMDMAVQIALQR 430
 Db 371 lrrllkeatfdgelelvrliinevklvnspgscfhcsepgwfrvcfnmdmtrialr 430
 QY 431 IRNFVLQNKVE--VVSNNKHCWNSNLRSLKTRFRDDITMSPHSPLPQSPMKV 481
 Db 431 irnfvlqtkglniaaikkcsrsklqislrldldfnspahspm--nslplr 482
 RESULT 7
 AAW52818
 ID AAW52818 standard; Protein: 504 AA.
 XX
 AC AAW52818;
 XX
 DT 07-JUL-1998 (first entry)

XX DE Coffee-fruit specific ACC synthase.
 XX DE
 XX KW Coffee-fruit; 1-aminocyclopropane-1-carboxylic acid synthase;
 KW ACC synthase; ethylene biosynthesis; fruit ripening.
 XX OS
 XX XX Coffea arabica.
 XX PN W09806852-A1.
 XX PD 19-FEB-1998.
 XX XX
 XX PF 11-AUG-1997; 97WO-US14184.
 XX PR 12-AUG-1996; 96US-0695412.
 XX PA (UYHA-) UNIV HAWAII.
 XX PI Moisyadi I, Neupane KR, Stiles JI;
 XX DR WPI; 1998-159543/14.
 XX DR N-PSDB; AAV20947.
 XX PT ACC synthase and ACC oxidase from coffee, Coffea arabica - and
 PT encoding DNA, useful in methods to control coffee bean ripening e.g.
 PT to allow synchronous ripening and thus more productive harvesting
 XX PS
 XX Claim 1; Fig 1; 72pp; English.
 XX CC The present sequence is Coffea arabica, coffee-fruit specific
 CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase.
 CC ACC synthase cDNA can be used to control ethylene biosynthesis in
 CC coffee plants, as ACC synthase is an element of the ethylene
 CC biosynthesis pathway. Transformation of wild-type coffee plants
 CC with constructs containing the cDNA in an antisense orientation
 CC can block ACC synthase synthesis. The cDNA can also be used to
 CC block ACC synthase synthesis by co-suppression. Plants transformed
 CC with the cDNA are incapable of synthesising ethylene, which is
 CC necessary in the final stages of fruit ripening in coffee,
 CC therefore ethylene application enables fruit ripening to be
 CC controlled, e.g. application to the entire plant can synchronise
 CC ripening. Coffee beans are preferably obtained from mature fruit,
 CC but non-uniform ripening has necessitated laborious hand-picking,
 CC or low yields and productivity when harvesting by strip harvesting
 CC or mechanical techniques. The ability to synchronise ripening
 CC makes mechanical harvesting more productive.
 XX SQ Sequence 504 AA;
 XX
 Query Match 69.0%; Score 1765; DB 19; Length 504;
 Best Local Similarity 65.3%; Pred. No. 6.6e-168;
 Matches 326; Conservative 83; Mismatches 66; Indels 24; Gaps 5;
 QY 7 DQPTLLSKMAIGDGHGESSPYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTSDLVEDW 66
 Db 8 eqqqlskmatndghenspyfdgkaydsdpybptrnpgvlgmglaenqlctdlleew 67
 QY 67 ILNPEASICTPEGINDFRAITANFDYHGLAEFRNAVAKFMARTGRNRTFDPDRIVMSG 126
 Db 68 vlnnpeasictaeganxfmevalyqdyhgypcfrqavarmekvrgdrvtfdpnrvmsg 127
 QY 127 GATGAHEVTAFLADPGEAFVLPIYPYPGFDRDLWRRTGKVLVPMCDSSNNFNLTKEAL 186
 Db 128 gatgahetlafcladpgeafvlptpypgfdrlwrtgmlpivcrssndfkvtkesm 187
 QY 187 EDAYEKAREDNIRVKGLLITNPNPLGTIMDRKTLRTVVSFINKRIHLVCEIYAATV 246
 Db 188 eayqkageanirvkfgllnnpnplgtvldretlglvtfndknhlcldeiyatsvf 247
 QY 247 SQPGFISATLEDETDECDRLNVHIVYSLSKDMGPPGFRVGIYISYNDVAVNCARKMS 306
 Db 248 sqpfeisiseih--dvqcnrdihivyslskdglfpgrvgyvlglysyndavvscarkms 305

SQ Sequence 486 AA;

Query Match 68.9%; Score 1762.5; DB 18; Length 486;
 Best Local Similarity 67.7%; Pred. No. 1:1e-167;
 Matches 325; Conservative 68; Mismatches 72; Indels 15; Gaps 3;

QY 8 QTPLLSKWAIGDGHGESSPYFDGHWKAYDQNPFFHTDNPNGVMQGLAENQLTSLDVEDWI 67
 DB 4 qhqlskiatndrgenspyfdgwkayknpfhtdnpdgvgimglaenqlsadiwi 63
 QY 68 LNPPEASICTPEGINDFRAITANFODYHGLAEFRNAVAKFARTGRNITFDPRIVMSGG 127
 DB 64 kkhpkasinepgevhmfkdlanfdyhgelpfrqaiakfmgvrgrvtdpdrivmsgg 123
 QY 128 ATGAHEVTACLDAPGBAFLVPIPYPGFDRDLRWRTGVKLVPVCMDCSSNNFVLTKEALE 187
 DB 124 atganellimcladpgdafivpspyafyrdlgwrtgvqvpvdcssnnfqtikvale 183
 QY 188 DAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDDEIYAATVES 247
 DB 184 aaydkaqgdglnvkgllitnpsnplgtldretikclisfineknhlvcddeiyaatifs 243
 QY 248 QPGFISAEILEDETDIECDRLNLIHVIYSLSKDMGFFGFRVGIYSYNDVAVNCARKMSS 307
 DB 244 sqnfsvseveevmd--cndrlhivyslekdmglpgfrvgivsyndavvncgrkms 301
 QY 308 FGLVSTOTQYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVIGIKCLOSNAGLFV 367
 DB 302 fglvssqtqyllasmladeefedflaesekrlkkrhgiftkgleqigiscleskaglfv 361
 QY 368 WMDLRQLLKPTFDSSETELMKVITHEVKINVSFGYSPCHTPEGFRVFCYANMDDMAYQIA 427
 DB 362 wmdlrlhllkeqtdngemelwrvindvknvpsgshfcvpgwfrvrcfammddetleiva 421
 QY 428 LQIRNEV-----LQNEVVYSNKKHCWHSNLRSLKTRRFD-----ITMSPHSPL 474
 DB 422 lkrthafveqekeretistktkdmptsktcwknlrfsfsrifeegigspiansphs 481

RESULT 10
 AA00985
 ID AAE00985 standard; Protein; 485 AA.
 AC AA00985;
 XX AA00985;
 DT 04-JUL-2001 (first entry)
 XX Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC 1A.
 DE Tomato; 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC 1A;
 KW ethylene production; fruit ripening; transgenic plant.
 XX Lycopersicon esculentum.
 OS
 XX US6207881-B1.
 PN
 XX 27-MAR-2001.
 PD
 XX 25-JAN-1995; 95US-0378313.
 PF
 XX 19-APR-1992; 92US-0862493.
 PR
 XX 10-SEP-1990; 90US-0579896.
 PP
 XX (USDA) US SEC OF AGRIC.
 PA
 XX Theologis A, Sato T;
 PI
 XX WPI; 2001-289591/30.
 XX Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic
 PT acid synthase, LE-ACC2 useful for producing ACC synthase which is
 PT essential for the production of ethylene in higher plants

XX Example 3; Fig 10; 92pp; English.
 XX The present sequence is tomato 1-aminocyclopropane-1-carboxylic acid
 CC synthase, LE-ACC 1A. ACC synthase are capable of catalysing the
 CC conversion of AdoMet (S-adenosyl methionine) to ACC and methyl
 CC thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which
 CC is essential for the production of ethylene in higher plants, where
 CC ethylene is a determinant of fruit ripening. The ACC DNA is also useful
 CC for producing transgenic plants which are overproducers of or are
 CC deficient in ACC synthase.
 XX SQ Sequence 485 AA;

Query Match 68.6%; Score 1755.5; DB 22; Length 485;
 Best Local Similarity 68.8%; Pred. No. 5.6e-167;
 Matches 327; Conservative 76; Mismatches 65; Indels 7; Gaps 5;

QY 11 LLSKWAIGDGHGESSPYFDGHWKAYDQNPFFHTDNPNGVMQGLAENQLTSLDVEDWILNN 70
 DB 13 llsklatndrgenspyfdgwkayannpffhtdnpdgvgimglaenqlcfldigewvwnn 72
 QY 71 PEASICTPEGINDFRAITANFODYHGLAEFRNAVAKFARTGRNITFDPRIVMSGGATG 130
 DB 73 pkasictvegaenfdiaiafdyhgelpfrqavafmekvrgvrtfdpnriivmsggatg 132
 QY 131 AHEVTACLDAPGBAFLVPIPYPGFDRDLRWRTGVKLVPVCMDCSSNNFVLTKEALEDAY 190
 DB 133 ahenlafcladpgdafivptpypgfdrdlrwtgvgqifpvvcescndfkvtkaaleay 192
 QY 191 EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDDEIYAATVFSQPG 250
 DB 193 ekaggsnikkgllitnpsnplgtldktdlrdvtfinsknihlvcddeiyaatvfdqpr 252
 QY 251 FISAEILEDETDIECDRLNLIHVIYSLSKDMGFFGFRVGIYSYNDVAVNCARKMSSRGL 310
 DB 253 fisvseivedm--lecnkdlhivyslekdmglpgfrvgivsyndvtnlarkmssrfgl 310
 QY 311 VSTOTQYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVIGIKCLOSNAGLFVMD 370
 DB 311 vstqthllasmladevfdkfaesserlgerqgmftkglaevgistklnagifvmd 370
 QY 371 LRQLLKPTFDSSETELMKVITHEVKINVSFGYSPCHTPEGFRVFCYANMDDMAYQIALQR 430
 DB 371 lrrllkeatfdelelwrllinevknvpsgshfcvpgwfrvrcfammddetmrlakr 430
 QY 431 IRNEVLQNKVE--VVSNNKKHCWHSNLRSLKTRRFD-DITMSP-HSPLPQSPMVK 481
 DB 431 isyfvlpqginniaaikkqcsrrklqislsfrldhefmspahspm-nspivr 484

RESULT 11
 AAB59723
 ID AAB59723 standard; Protein; 485 AA.
 XX AAB59723;
 AC AAB59723;
 XX 29-MAR-2001 (first entry)
 DT
 XX Tomato ACC synthase gene LE-ACC1A(b) clone.
 DE
 XX ACC synthase; 1-aminocyclopropane-1-carboxylic acid synthase; enzyme;
 KW ethylene production; fruit ripening; tomato; LE-ACC.
 XX Lycopersicon esculentum.
 OS
 XX US6156956-A.
 PN
 XX 05-DEC-2000.
 PD
 XX 02-MAR-1998; 98US-0033349.
 PF
 XX

PR 25-JAN-1995; 95US-0378313.
PR 02-APR-1992; 92US-0862493.
PR 07-JUN-1995; 95US-0481171.
PR 10-SEP-1990; 90US-0579896.
PA (USDA) US DEPT OF AGRICULTURE.
XX Sato T, Theologis A;
XX WPI; 2001-079558/09.
XX Expression cassette for producing transgenic plants exhibiting
PT inhibited ethylene production and delayed fruit ripening, comprises
PT complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic acid
PT synthase synthesis -
XX
XX Example 3; Fig 10; 91pp; English.
XX
XX 1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for
CC the production of ethylene in higher plants; ethylene is a determinant
CC of fruit ripening. The present invention relates to an expression
CC cassette which comprises the reverse transcript of RNA complementary to
CC an RNA transcribed from ACC synthase gene. The expression cassette can be
CC used to prevent ACC gene expression. The expression cassette is useful
CC for inhibiting ethylene production and fruit ripening, when introduced
CC into a plant or plant cells. The present sequence is the protein encoded
CC by tomato ACC synthase gene LE-ACC1A(b) clone. This sequence was used in
CC a sequence homology comparison with other ACC synthase gene clones
CC (AAB59721-B59727).
XX
XX Sequence 485 AA;
XX
Query Match 68.6%; Score 1755.5; DB 22; Length 485;
Best Local Similarity 68.8%; Pred. No. 5.6e-167;
Matches 327; Conservative 76; Mismatches 65; Indels 7; Gaps 5;
QY 11 LLSKMAIGDHGESSPYFDGWKAYDONPPHPTDNPNGVMQGLAENQLTSDLVEDWILNN 70
DB 13 llsklatndghgensepyfdgwkayannphtldnptgviqmglaenqlcfdlqewvwnn 72
QY 71 PRASICTPGINDFRAIANFQDYHGLAEFRNAVAKFMATRGNRITFDPRIVMSGGATG 130
DB 73 pkractvegaenfdiaifqdyhglpeirqavarfmekevrgdrvtfdpnrivmssgagc 132
QY 131 AHEVTAFLADPGEAFLVPIPYPGFDRDLRWRTGKLVPMCDSSNNFVLTKAELEDAY 190
DB 133 ahemlafcladpgdaflvptpygfdrlrwtgvlfpvvescndfkvttkaleey 192
QY 191 EKAREDNIKVGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDIYAATVFSQPG 250
DB 193 ekaqgsnkikgllnnpsnplgtildktdrdivtflnsknhlvcdeiyaatvfdqpr 252
QY 251 FTSIARILEDETDICDRNLHVIVSLSDMGFPGRVGIYISYNDVAVNCARKMSSFGL 310
DB 253 flsvseivedm--iecnkdilhlvyslkdglfpgrvgyvsvndvtnlarkmssfgl 310
QY 311 VSTQYQYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGLAKRVGKICLQSNAGLFVWMD 370
DB 311 vstqqtqhlhllasmldsevfdkfiaesserlgerqgmftkgaevgistlksnaglfvwm 370
QY 371 LRQLLKPTFDETEFLWKVIIIEVKINVSFGYSEFCTEPCWFRVCYANNMDMAVQIALQR 430
DB 371 lrrllkeatfdelelwrllievklnvsgpghcsepgvfrvcfanmdetmrlakr 430
QY 431 IRNFVLQKREV--VVSNNKKHCHNSLRSLKTRRFD-DITMSP-RHSPQSPWVK 481
DB 431 isyfvlpqkglaniaalkqcsrrklqslsfrldhefmsnspahpm-nslpr 484
RESULT 12
AAR15508
ID AAR15508 standard; Protein; 485 AA.

XX AAR15508;
XX 17-DEC-2001 (updated)
XX 09-MAR-1992 (first entry)
XX Tomato ACC synthase encoded by clone LE-ACC1A.
XX 1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening.
XX Lycopersicon esculentum c.v. Rutgers.
XX USN7579896-N.
XX 12-NOV-1991.
XX 10-SEP-1990; 90US-0579896.
XX 10-SEP-1990; 90US-0579896.
XX (USDA) US SEC OF AGRICULTURE.
XX Theologis A, Sato T;
XX WPI; 1991-368895/50.
XX DNA encoding ACC synthase - used for control of plant development
XX and for prodn. of ACC synthase, ethylene and ethanol
XX Disclosure; Fig 14; 73pp; English.
XX Genomic clone LE-ACC1A was one of four different clones identified
CC in a library prepared from total DNA extracted from etiolated Rutgers
CC seedlings. Screening was by the cDNA clone pACC1 (see AAQ15134). The
CC amino acid sequence was deduced from the cDNA and shows
CC considerable homology with ACC sequences deduced from the three other
CC tomato and the zucchini clones.
CC See AAQ15131-Q15140.
CC (Note: Revised entry submitted to correct the patent number format of
CC US Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)
XX Sequence 485 AA;
XX
Query Match 68.2%; Score 1746.5; DB 12; Length 485;
Best Local Similarity 68.6%; Pred. No. 4.5e-166;
Matches 326; Conservative 76; Mismatches 66; Indels 7; Gaps 5;
QY 11 LLSKMAIGDHGESSPYFDGWKAYDONPPHPTDNPNGVMQGLAENQLTSDLVEDWILNN 70
DB 13 llsklatndghgensepyfdgwkayannphtldnptgviqmglaenqlcfdlqewvwnn 72
QY 71 PRASICTPGINDFRAIANFQDYHGLAEFRNAVAKFMATRGNRITFDPRIVMSGGATG 130
DB 73 pkractvegaenfdiaifqdyhglpeirqavarfmekevrgdrvtfdpnrivmssgagc 132
QY 131 AHEVTAFLADPGEAFLVPIPYPGFDRDLRWRTGKLVPMCDSSNNFVLTKAELEDAY 190
DB 133 ahemlafcladpgdaflvptpygfdrlrwtgvlfpvvescndfkvttkaleey 192
QY 191 EKAREDNIKVGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDIYAATVFSQPG 250
DB 193 ekaqgsnkikgllnnpsnplgtildktdrdivtflnsknhlvcdeiyaatvfdqpr 252
QY 251 FTSIARILEDETDICDRNLHVIVSLSDMGFPGRVGIYISYNDVAVNCARKMSSFGL 310
DB 253 flsvseivedm--iecnkdilhlvyslkdglfpgrvgyvsvndvtnlarkmssfgl 310
QY 311 VSTQYQYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGLAKRVGKICLQSNAGLFVWMD 370
DB 311 vstqqtqhlhllasmldsevfdkfiaesserlgerqgmftkgaevgistlksnaglfvwm 370

CC linked to control sequences that effect its transcription into the
CC antisense RNA, where the cDNA can be amplified from the endogenous
CC ACC synthase gene by primer pairs encoding conserved ACC synthase
CC sequences. The DNA molecule can be used to delay ripening of
CC tomato or zucchini fruits.

[illegible]

RESULT 15	
AAE00984	
ID	AAE00984 standard; Protein; 485 AA.
XX	
XX	
AC	AAE00984;
XX	
XX	
DT	04-JUL-2001 (first entry)
XX	
DE	Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2.
XX	
KW	Tomato; 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC2;
KW	ethylene production; fruit ripening; transgenic plant.
XX	
XX	
OS	Lycopersicon esculentum.
XX	
XX	
Key	Location/Qualifiers
PH	
FT	Misc-difference 124
FT	/note= "Encoded by GTT; this translation exception
FT	occurs while decoding LE-ACC2 CDNA (AA004546)."
FT	

US6207881-B1.

27-MAR-2001.

Search completed: August 21, 2002, 02:08:07

Job time: 6087 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
Run on: August 21, 2002, 02:08:55 ; Search time 24.39 Seconds
(without alignments)
768.358 Million cell updates/sec
Title: US-09-763-957-2
Perfect score: 2559
Sequence: 1 MGFKAMDQPLLSKMAIGDG.....DITMSPHSLPQSPVWKATN 484
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	2354	92.0	484	1	1A1C_SOYBN	P31531 glycine max
2	1927	75.3	368	1	1A1C_PHAU	O01912 phaseolus a
3	1739.5	68.0	491	1	1A1C_TOBAC	O07262 nicotiana t
4	1713	66.9	485	1	1A12_LYCES	P18485 lycopersico
5	1698.5	66.4	492	1	1A11_PPRUM	Q9MB95 prunus mume
6	1640.5	64.1	493	1	1A11_CUCMA	P23599 cucurbita m
7	1637.5	64.0	493	1	1A11_CUCPE	P23279 cucurbita p
8	1627.5	63.6	494	1	1A12_CUCPE	O00379 cucurbita p
9	1603.5	62.7	517	1	1A1C_DIACA	P27486 dianthus ca
10	1584	61.9	476	1	1A14_LYCES	P29535 lycopersico
11	1578	61.7	496	1	1A12_ARATH	Q06402 arabidopsis
12	1341	52.4	473	1	1A1C_MALDO	P37821 malus domes
13	1339.5	52.3	475	1	1A12_CUCMA	Q00257 cucurbita m
14	1258.5	49.2	487	1	1A11_ORYSA	O07215 oryza sativ
15	293.5	11.5	394	1	AAT_AQUAE	O67781 aquifex aeo
16	276.5	10.8	392	1	AAT_BACSP	P23034 bacillus sp
17	274.5	10.7	397	1	AAT_STRVG	Q60013 streptomyce
18	263	10.3	392	1	PATA_BACSU	P16524 bacillus su
19	256.5	10.0	393	1	AAT1_BACSU	P53001 bacillus su
20	252	9.8	370	1	AAT2_METJA	Q58097 methanococ
21	248.5	9.7	393	1	AAT_BACST	Q59228 bacillus st
22	248	9.7	377	1	AAT_THEMA	Q9X0Y2 thermotoga
23	229	8.9	412	1	AAT_RICPR	Q9ZE56 rickettsia
24	227	8.9	389	1	AAT_PYRAB	Q9V012 pyrococcus
25	225.5	8.8	410	1	AAB1_RHIME	P58350 rhizobium m
26	225	8.8	383	1	AAT_THAQ	Q33822 thermus aqu
27	224	8.8	416	1	AAT1_TRYCR	P33447 trypanosoma
28	222.5	8.7	410	1	AAB2_RHIME	Q06191 rhizobium m
29	220.5	8.6	399	1	AAT2_BACSU	P39643 bacillus su
30	220	8.6	482	1	ALA2_PANMI	P34106 panicum mil
31	217.5	8.5	482	1	ALA2_HORVU	P52894 hordeum vul
32	217	8.5	385	1	AAT_THETH	Q56232 thermus aqu
33	216.5	8.5	429	1	AAT_MYCTU	O33267 mycobacteri

P52892 saccharomyc
P04694 rattus norv
P77434 escherichia
P24298 homo sapien
P77727 escherichia
P71348 haemophilus
P17735 homo sapien
Q10334 schizosacch
P52893 saccharomyc
O38489 pyrococcus
Q55128 synechocyst
Q60317 methanococc

ALIGNMENTS

RESULT 1
1A1C_SOYBN STANDARD; PRT; 484 AA.
AC P31531;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACS1;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CENTURY; TISSUE=Leaf;
RA Liu D, Li N, Mattos A, K
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine -> L-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL; X67100; CAA47474.1;
CC PIR; S25002; S25002.
CC HSP; P37821; I188.
CC Mendel; 8361; GLYMa; Accs;1.
CC InterPro; IPR001176; ACC-synthase.
CC Pfam; PF00155; aminotran_1.2; 1.
CC PRINTS; PR00753; ACCSYNTHASE.
CC PROSITE; PS00105; AA-TRANSFER CLASS.1; 1.
CC Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
CC Multigene family. 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT BINDING .279 279
SQ SEQUENCE 484 AA; 54730 MW; 152F7AD12B992987 CRC64;

Query Match 92.0%; Score 2354; DB 1; Length 484;
Best Local Similarity 90.9%; Pred. No. 4.5e-174;
Matches 439; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY 1 MGFRAMDTPLLSKMAIGDHGESSPYFDGKAYDQNFPHFTDNPNGVMQGLAENQLTS 60
DB 1 MGLMDVDQTQLLSKMAIGDHGESSPYFDGKAYDQNFPHFTDNPNGVMQGLAENQLTS 60
QY 61 DLVEDWILNNEPASICCTEGINDFRAIANFQDYGHLAEFRNAVAKFMRNRTFPDP 120
DB 61 DLVEDWILNNEPASICCTEGINDFRAIANFQDYGHLAEFRNAVAKFMRNRTFPDP 120
QY 121 RIVMSGGATGAHEVTAFCADPGAEAFVPIPYPGFDRDLRWRTGKLVPMVCDSSNNFV 180
DB 121 RIVMSGGATGAHEVTAFCADPGAEAFVPIPYPGFDRDLRWRTGKLVPMVCDSSNNFV 180
QY 181 LTKALEDAYEKAREDNIRVKGLLITNPSPGLTMDRKTLLRTVVSFNEKRIHLVCD 240
DB 181 LTKALEDAYEKAREDNIRVKGLLITNPSPGLTMDRKTLLRTVVSFNEKRIHLVSD 240
QY 241 YAATVFSQPGFISIAEILEDDETDICDRNLVHIVYSLSKDMGFGFRGVIIYSYND 300
DB 241 YSATVFSHPSTISIAEILEDDETDICDRNLVHIVYSLSKDMGFGFRGVIIYSYND 300
QY 301 CARMKSSFGVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTGGGLAKVGKICLQ 360
DB 301 CARMKSSFGVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTGGGLAKVGKICLQ 360
QY 361 SNAGLFVWMDLRQLLKKPTFSETELWKVIIHEVKINSPGYSFHCFTPGFVRVCYAN 420
DB 361 SNAGLFVWMDLRQLLKKPTFSETELWKVIIHEVKINSPGYSFHCFTPGFVRVCYAN 420
QY 421 DNVAQIALQIRINFLQNKVVVKNKCHWSNLRLSKLTKTRFDDITWSPHPLQSPMV 480
DB 421 DNVAQIALQIRINFLQNKVVVKNKCHWSNLRLSKLTKTRFDDITWSPHPLQSPMV 480
QY 481 KAT 483
DB 481 KAT 483

RESULT 2
ID 1A1C PHAAU STANDARD; PRT; 368 AA.
AC Q01912;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC
DE synthase) (S'-adenosyl-L-methionine methylthioadenosine-lyase)
DE (Fragment).
CN ACS5.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. BERKEN / RWILC2; TISSUE=Hypocotyl;
RX MEDLINE=93043033; PubMed=1421146;
RA Botella J.R., Arteca J.M., Schlaghauser C.D., Arteca R.N.,
RA Phillips A.T.;
RT "Identification and characterization of a full-length cDNA encoding
RT for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from
RT etiolated mung bean hypocotyl segments and expression of its mRNA in
RT response to indole-3-acetic acid.";
RL Plant Mol. Biol. 20:425-436(1992).
CC 1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC 1- CATALYTIC ACTIVITY: S'-adenosyl-L-methionine + methylthioadenosine.
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC 1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC 1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC 1- SURUNIT: HOMODIMER.
CC 1- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS

CC MECHANICAL WOUNDING AND A NUMBER OF CHEMICALS.
CC 1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; Z11562; CAA77655.1; -
DR HSSP; P37821; 1B8G.
DR Mendel; 9876; PHAAU; Acs; 5.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF001155; aminotran_1.2; 1.
DR PROSITE; PS00105; AA-TRANSFER-CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT NON_TER 1
FT BINDING 230 230
FT NON_TER 368 368
SQ SEQUENCE 368 AA; 41477 MW; 31BA61D5FC2DACB8 CRC64;
Query Match 75.3%; Score 1927; DB 1; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.6e-141;
Matches 367; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 50 QMGLAENQLTSLVEDWILNNEPASICCTEGINDFRAIANFQDYGHLAEFRNAVAKFMR 109
DB 1 QMGLAENQLTSLVEDWILNNEPASICCTEGINDFRAIANFQDYGHLAEFRNAVAKFMR 60
QY 110 TRGNRTITFDPRIVMSGGATGAHEVTAFCADPGAEAFVPIPYPGFDRDLRWRTGKLV 169
DB 61 TRGNRTITFDPRIVMSGGATGAHEVTAFCADPGAEAFVPIPYPGFDRDLRWRTGKLV 120
QY 170 PYMCDSSNNFVLTKEALDAYEKAREDNIRVKGLLITNPSPGLTMDRKTLLRTVVSFN 229
DB 121 PYMCDSSNNFVLTKEALDAYEKAREDNIRVKGLLITNPSPGLTMDRKTLLRTVVSFN 180
QY 230 EKRIHLVCDIYAATVFSQPGFISIAEILEDDETDICDRNLVHIVYSLSKDMGFGFRVG 289
DB 181 EKRIHLVCDIYAATVFSQPGFISIAEILEDDETDICDRNLVHIVYSLSKDMGFGFRVG 240
QY 290 IYISYNDVAVNCARKMSFGLVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTG 349
DB 241 IYISYNDVAVNCARKMSFGLVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTG 300
QY 350 GLAKVGKICLQSNAGLFVWMDLRQLLKKPTFSETELWKVIIHEVKINSPGYSFHCFT 409
DB 301 GLAKVGKICLQSNAGLFVWMDLRQLLKKPTFSETELWKVIIHEVKINSPGYSFHCFT 360
QY 410 GWFRCVYA 417
DB 361 GWFRCVYA 368
RESULT 3
ID 1A1C_TOBAC STANDARD; PRT; 491 AA.
AC Q07262;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC
DE synthase) (S'-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACS1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

```
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. XANTHI;
RA Bailey B.A., Avni A., Li N., Matoo A.K., Anderson J.D.;
RT "Nucleotide sequence of the Nicotiana tabacum cv xanthi gene encoding
RL Plant Physiol. 100:1615-1616(1992).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X5982; CAA46797.1; -.
CC HSSP; P37821; 1B8G.
CC Mendel; 252; NICta; Acs;1.
CC InterPro; IPR001176; ACC_synthase.
CC InterPro; IPR001511; Aminotran.1.
CC Pfam; PF00155; aminotran.1.2; 1.
CC PRINTS; PR00753; ACCSYNTHASE.
CC PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
CC Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate.
KW BINDING 278 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 491 AA; 55290 MW; 57B9FF4306686DFD CRC64;
SQ
Query Match 68.0%; Score 1739.5; DB 1; Length 491;
Best Local Similarity 66.5%; Pred. No. 1.1e-126;
Matches 326; Conservative 71; Mismatches 84; Indels 9; Gaps 5;
QY 1 MGFANDQTPLLSKMAIGDGHGESSYFDGKAYDQNPDPHTDPNGVMQGLAENQLTS 60
DB 1 MGFENEKNSILSKLATNEELGNSYFDGKAYDNDPPLKPNKPNQVGMGLAENQLCF 60
QY 61 DLVEDWILNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKEMARTGRNRTFDPD 120
DB 61 DLIEWIKRNPASICTTEGKSFRAIANFQDYHGLAEFRNAVAKEMARTGRNRTFDPD 120
QY 121 RYVMSGGATGAHEVTAFCADPGAEFLVPIPYYPGDFDRDLRWRTGTVKLVPMCDSSNNFV 180
DB 121 RYVMAGGATGANETIIFCLADTGAELVSPYPYPAFNRLDLRWRTGTVQLPIPCDSSNNFQ 180
QY 181 LKFEALDAYEKAREDIRVKGILLINPSNPIGTMIDRKLTRVSVFNEKRLHLCVDEI 240
DB 181 ITTKAVREAYEAKNSIKVKGILLINPSNPLGTTDLRDLTKLLFTNOHNLHLCVDEI 240
QY 241 YAATVFSQPGFISAIIELEDETIEDCDRLNHLVHIVYSLSKDMGPPGPRVGIYSYNDAVNV 300
DB 241 YAATVNTQFVSAIILDDETS-HCNKDLVHIVYSLSKDMGLPGRVGLVYSFNDAVNV 299
QY 301 CARMKSSFGVLSTQTOYLLASMLNDDDEFERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
DB 300 CARMKSSFGVLSTQTOYLLAEMLSDERFSNFTLESSKRLAKRKHFTNGLEVGKCLR 359
QY 361 SNAGLFWMDLRLKLPKPFDSSTELWKYIIIEVKLVNSPGYFHCFTPEQFWFRVCANMD 420
DB 360 SNAGLFCWMDRLPLKESFDSMSLWRVINDVKLVNSPGSSFDQCEQGFVRVCANMD 419
QY 421 DMAVQIALQIRNFVLQNE-----VYVSNKKHCW-HSNLRLSLKTRRFD-ITMSP-HS 472
DB 421 DMAVQIALQIRNFVLQNE-----VYVSNKKHCW-HSNLRLSLKTRRFD-ITMSP-HS 472
Db 420 DETVDIALAIRSFVGVKSGDESTPILMEKKQOWKKNLRLSFSKRMYSYNLSPSS 479
QY 473 PLPQSPMWKA 482
Db 480 PIPHSPLVRA 489
RESULT 4
ID 1A12_LYCES STANDARD; PRT; 485 AA.
AC P1B485;
DC 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase 2 (EC 4.4.1.14) (ACC
DE synthase 2) (S-adenosyl-L-methionine methylthioadenosine-lyase 2)
DE (ACS-2).
GN ACS2 OR PCVW4A.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Etolated hypocotyl;
RX MEDLINE=92106351; PubMed=1762159;
RA Rottmann W.H., Peter G.F., Oeller P.W., Keller J.A., Shen N.F.,
RA Nagy B.P., Taylor L.P., Campbell A.D., Theologis A.;
RT "1-aminocyclopropane-1-carboxylate synthase in tomato is encoded by a
RT multigene family whose transcription is induced during fruit and
RT floral senescence.";
RL J. Mol. Biol. 222:937-961(1991).
RN [2]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC STRAIN=CV. ORLANDO; TISSUE=Fruit;
RX MEDLINE=90280476; PubMed=2191304;
RA van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;
RT "Cloning and sequence of two different cDNAs encoding 1-
RT aminocyclopropane-1-carboxylate synthase in tomato.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:4859-4863(1990).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS
CC MECHANICAL WOUNDING AND A NUMBER OF CHEMICALS.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X59139; CAA41855.1; -.
CC EMBL; X59145; CAA41856.1; -.
CC EMBL; M34289; AAA81580.1; -.
CC PIR; S19677; S19677.
CC PIR; S19678; S19678.
CC PIR; A35516; A35516.
CC HSSP; P37821; 1B8G.
CC Mendel; 509; LYCES; Acs;2.
CC InterPro; IPR001176; ACC_synthase.
CC InterPro; IPR001511; Aminotran.1.
CC Pfam; PF00155; aminotran.1.2; 1.
CC PRINTS; PR00753; ACCSYNTHASE.
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DR PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 124 A -> V (IN REF. 1; CAA41856).
FT CONFLICT 322 L -> P (IN REF. 2).
FT CONFLICT 399 P -> L (IN REF. 2).
SQ SEQUENCE 485 AA; 54662 MW; 40B3F55B5EF0D9C7 CRC64;

Query Match 66.9%; Score 1713; DB 1; Length 485;
Best Local Similarity 65.6%; Pred. No. 1.2e-124;
Matches 319; Conservative 72; Mismatches 89; Indels 6; Gaps 4;

QY 1 MGFKAMDQTPLLSKMAIGDHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTS 60
DB 1 MGFETAKTNSILSKLATNEHCENSPPYFDGWKAYDSDPFHPLKPNPVGVIOMGLAENQLCL 60

QY 61 DLVDEWILNPPASICTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNRTTFDPPD 120
DB 61 DLIEDWIKRNKPGSICS-EGIKSPKAIANFQDYGHLPEFRKAIAKMEKTRGGRVRFDPPE 119

QY 121 RIVMSGGATGAHEVTAFCADLADGPEAFPIPIYPYPGFDRDLRWRGTVKLVPMCDSSNNFV 180
DB 121 RIVMSGGATGAHEVTAFCADLADGPEAFPIPIYPYPGFDRDLRWRGTVKLVPMCDSSNNFV 180

QY 120 RVVAGGATGANETIIFCLADPGDAFLVPSPIYPFAPFNDRDLRWRGTVQLPIHCESNNFK 179
DB 120 RVVAGGATGANETIIFCLADPGDAFLVPSPIYPFAPFNDRDLRWRGTVQLPIHCESNNFK 179

QY 181 LKAELEDAYEKAREDNIRVKGLLTNPSPNLGTIMDKRTLTVVVSFNEKRIHLVCDDEI 240
DB 181 LKAELEDAYEKAREDNIRVKGLLTNPSPNLGTIMDKRTLTVVVSFNEKRIHLVCDDEI 240

QY 180 ITS KAVKAYENAKSKVKGLLTNPSPNLGTITLTKSLVSLFTNOHNIHLVCDDEI 239
DB 180 ITS KAVKAYENAKSKVKGLLTNPSPNLGTITLTKSLVSLFTNOHNIHLVCDDEI 239

QY 241 YAATVPSQPGFTSIAEILEDDETDICDRNLHIVYSLSKDMGFGPFRVGIYSYNDVAVN 300
DB 241 YAATVPSQPGFTSIAEILEDDETDICDRNLHIVYSLSKDMGFGPFRVGIYSYNDVAVN 300

QY 240 YAATVFDTPQFYSIAEILEDQEMTYCNKDLHVIVYSLSKDMGLPGFRVGIYSFNDVAVN 299
DB 240 YAATVFDTPQFYSIAEILEDQEMTYCNKDLHVIVYSLSKDMGLPGFRVGIYSFNDVAVN 299

QY 301 CARKMSSFGLVSTQYQLLASMLNDEFEVERELASAKRLAQRFRVFTGGLAKVGKICLQ 360
DB 301 CARKMSSFGLVSTQYQLLASMLNDEFEVERELASAKRLAQRFRVFTGGLAKVGKICLQ 360

QY 300 CARKMSSFGLVSTQYQLLASMLNDEFEVERELASAKRLAQRFRVFTGGLAKVGKICLQ 359
DB 300 CARKMSSFGLVSTQYQLLASMLNDEFEVERELASAKRLAQRFRVFTGGLAKVGKICLQ 359

QY 361 SNAGLFWMDLRQLKPTFSETELWKVIIEVKINSPGYSFHCETEPGFRVCIYANND 420
DB 361 SNAGLFWMDLRQLKPTFSETELWKVIIEVKINSPGYSFHCETEPGFRVCIYANND 420

QY 360 NNAGLFCWMDLRQLKPTFSETELWKVIIEVKINSPGYSFHCETEPGFRVCIYANND 419
DB 360 NNAGLFCWMDLRQLKPTFSETELWKVIIEVKINSPGYSFHCETEPGFRVCIYANND 419

QY 421 DNAYOIALQIRINFLQNKKEVVSNN---KKHCW-HSNRLSLKTRFRDDITNSP-HSLPLP 475
DB 421 DNAYOIALQIRINFLQNKKEVVSNN---KKHCW-HSNRLSLKTRFRDDITNSP-HSLPLP 475

QY 476 QSPMYK 481
DB 476 QSPMYK 481

QY 480 PSPLVR 485
DB 480 PSPLVR 485

RESULT 5
1A11_PRUMU STANDARD; PRT; 492 AA.
AC Q9MB95;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACSL.
OS Prunus mume (Japanese flowering apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=102107;
RN [1]
RP SEQUENCE FROM N.A.
RA Mita S., Kirita C., Kato M., Hyodo H.;
RT *Expression of ACC synthase is enhanced earlier than that of ACC
RT oxidase during fruit ripening of mume (Prunus mume)*;
RL Physiol. Plantarum 107:319-328(1999).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
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CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine -> L-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COPACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB031026; BAA05049.1; -.
CC InterPro; IPR001176; ACC_synthase.
CC InterPro; IPR001511; Aminotran_1.
CC Pfam; PF00155; aminotran_1.2; 1.
CC PRINTS; PR00753; ACCSYNTHASE.
CC PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 492 AA; 55066 MW; 2002047AF2B43D89 CRC64;

Query Match 66.4%; Score 1698.5; DB 1; Length 492;
Best Local Similarity 66.6%; Pred. No. 1.6e-123;
Matches 321; Conservative 62; Mismatches 86; Indels 13; Gaps 4;

QY 11 LLSKMAIGDHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTSDFSDIEWIKLN 70
DB 11 LLSKMAIGDHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTSDFSDIEWIKLN 70

QY 12 LLSKATSEGHEGNSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTSDFSDIEWIKLN 71
DB 12 LLSKATSEGHEGNSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTSDFSDIEWIKLN 71

QY 71 PEASICTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNRTTFDPRVMSGGATG 130
DB 71 PEASICTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNRTTFDPRVMSGGATG 130

QY 72 PRASICTPEGVEEFKNVAIFQDYGHLAEFRNAVAFMARTGRNRTTFDPRVMSGGATG 131
DB 72 PRASICTPEGVEEFKNVAIFQDYGHLAEFRNAVAFMARTGRNRTTFDPRVMSGGATG 131

QY 131 AHEVTAFCADLADGPEAFPIPIYPYPGFDRDLRWRGTVKLVPMCDSSNNFVLTKEALEAY 190
DB 131 AHEVTAFCADLADGPEAFPIPIYPYPGFDRDLRWRGTVKLVPMCDSSNNFVLTKEALEAY 190

QY 132 ANELVMFCADLADGDAFLVPSPIYPFAPFNDRDLRWRGTVKLVPMCDSSNNFVLTKEALEAY 191
DB 132 ANELVMFCADLADGDAFLVPSPIYPFAPFNDRDLRWRGTVKLVPMCDSSNNFVLTKEALEAY 191

QY 191 EKAREDNIRVKGLLTNPSPNLGTIMDKRTLTVVVSFNEKRIHLVCDDEIYAATVFSOPG 250
DB 191 EKAREDNIRVKGLLTNPSPNLGTIMDKRTLTVVVSFNEKRIHLVCDDEIYAATVFSOPG 250

QY 192 EKAQANNINVKGLIITNPSPNLGTITLDRNTLESLEFFINQKNIHLVCDDEIYAATVFSPT 251
DB 192 EKAQANNINVKGLIITNPSPNLGTITLDRNTLESLEFFINQKNIHLVCDDEIYAATVFSPT 251

QY 251 FTISAEILEDDETDICDRNLHIVYSLSKDMGFGPFRVGIYSYNDVAVNCARKMSSFG 310
DB 251 FTISAEILEDDETDICDRNLHIVYSLSKDMGFGPFRVGIYSYNDVAVNCARKMSSFG 310

QY 252 FTCSIEVIQ---NMNCNPNLHIVYSLSKDMGLPGLRVGIYVNDVAVNICKRMSSFG 308
DB 252 FTCSIEVIQ---NMNCNPNLHIVYSLSKDMGLPGLRVGIYVNDVAVNICKRMSSFG 308

QY 311 VSTOYQLLASMLNDEFEVERELASAKRLAQRFRVFTGGLAKVGKICLOSAGLFWMD 370
DB 311 VSTOYQLLASMLNDEFEVERELASAKRLAQRFRVFTGGLAKVGKICLOSAGLFWMD 370

QY 309 VSSQTHMLPSMLLDEEFVAREFTSPKRLAKRHGVTFTKGLVEEVNCLKSLAGLFCWMD 368
DB 309 VSSQTHMLPSMLLDEEFVAREFTSPKRLAKRHGVTFTKGLVEEVNCLKSLAGLFCWMD 368

QY 371 LRQLLKPTFSETELWKVIIEVKINSPGYSFHCETEPGFRVCIYANNDNAVOIALQ 430
DB 371 LRQLLKPTFSETELWKVIIEVKINSPGYSFHCETEPGFRVCIYANNDNAVOIALQ 430

QY 369 LRRLLDQTFDGEVWLVRVINEVGNVSPGSSFKCEVGEFRVCFANMDDTLEVALKR 428
DB 369 LRRLLDQTFDGEVWLVRVINEVGNVSPGSSFKCEVGEFRVCFANMDDTLEVALKR 428

QY 431 TRNFVLQNK----EVVSNKKHCWHSNRLSL---KTRFRDDIT---MSPHSPPLPSPMY 480
DB 431 TRNFVLQNK----EVVSNKKHCWHSNRLSL---KTRFRDDIT---MSPHSPPLPSPMY 480

QY 429 INTFVROGKAQDQVQVQVQKSPKRWKSNLRLSPSSSTRFRDQESVNLSPHMSPLV 488
DB 429 INTFVROGKAQDQVQVQVQKSPKRWKSNLRLSPSSSTRFRDQESVNLSPHMSPLV 488

QY 481 KA 482
DB 481 KA 482

QY 489 RA 490
DB 489 RA 490

RESULT 6
1A11_CUCMA STANDARD; PRT; 493 AA.
ID 1A11_CUCMA
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AC P23599;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase CWM33 (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACS1 OR ACCW.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakajima N., Mori H., Yamazaki K., Imaseki H.;
RT "Molecular cloning and sequence of a complementary DNA encoding 1-
RT aminocyclopropane-1-carboxylate synthase induced by tissue wounding.";
RL Plant Cell Physiol. 31:1021-1029(1990).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- INDUCTION: BY TISSUE WOUNDING.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; D01032; BAA00838.1; -
DR PIR; JQ0926; JQ0926.
DR KSP; P37821; 186G.
DR Mendl; 244; CUCma; Accs;1.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran.1.
DR Pfam; PF00155; aminotran.1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 279 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 493 AA; 55895 MW; F39234AC99CBEF6B CRC64;

Query Match 64.1%; Score 1640.5; DB 1; Length 493;
Best Local Similarity 63.2%; Pred. No. 4.8e-119;
Matches 313; Conservative 74; Mismatches 95; Indels 13; Gaps 6;

QY 1 MGFAMQD--TPLLSKAIGDGHGESSPYFDGKAYDQNFPHPTDNPNGVMQGLAENQL 58
DB 1 MEFHQIDERNQALLSKIAVDGNGHSPYFDGKAYDNDPFPHPDNPNGVMQGLAENQL 60
QY 59 TSLDVEDWLNPEASICTPEGINDFRAINFQDYGHLAEFRNAVAKFMARTGRNRTED 118
DB 61 SFDIVDWIKRHPASICTPGLERFKSIANFQDYGHLPEFRNGIASFMGKVRGRVQFD 120
QY 119 PDRIVMSGGATGAHEVTAFLADPGEAFVPIPIYPGDFDRDLRWRTGKVLPPVMDSSNN 178
DB 121 PSRIVMSGGATGASSETVIFCLADPGDAFLVPSPYAAFDRLKWRTRAQIIRVHCNSSNN 180
QY 179 FVLTKALEADAYEKARDNTIRVGLLTITNPSNPLGTTMDRKTLRTVVSFNEKRHLVCD 238
DB 181 FOVTKAALETAYKKAQGANIKVRGVIITNPSNPLGTTMDRKTLRTVVSFNEKRHLVCD 240
QY 239 EIVAATVFSQPGFISIAIELEDIEDCNRLNHLVIVYSLSKDNGFPGRFRVGIISYNDV 298

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Db 241 EIVSATVFKAPTFTISIAQIVEEME--HCKELIHLISLSKDMGLPGFRVGIISYNDV 298
QY 299 VNCARKMSFGLVSTQTYLIASMLNDEFERFLAESAARLAQFRVFTTGLAKVGIKC 358
Db 299 VRRARQMSFGLVSSQTHLLAAMLSDDEDVDFKFLAENSRLAERHARFTKELDKMGITC 358
QY 359 LOSNAGLVFVMDLRQLLKKPTFDSSETELKVIIEVINSPGYSFHCTEGPWRVCYAN 418
Db 359 LNSNAGVFVMDLRRLKDKDTFAEMELWRVVIINEVKLVNPGSSFHVTEPGWFRVCAN 418
QY 419 MDDMAVOIALQIRNEV--LQNKEL--VVSNNKCHWHSNLR--SLKTRFED--ITMS 469
Db 419 MDDNTVDVALNRHISFVENIDKEDNTVAMPKTRRRNKLRSFSFGRRYDEGNVLS 478
QY 470 PHSPLQSPVMKATN 484
Db 479 PHTMSPHSPVIAKN 493

RESULT 7
LAIL_CUCPE STANDARD; PRT; 493 AA.
AC P23279;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACC1A.
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3663;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91139670; PubMed-1995630;
RA Sato T., Oeller P.W., Theologis A.;
RT "The 1-aminocyclopropane-1-carboxylate synthase of Cucurbita.
RT Purification, properties, expression in Escherichia coli, and primary
RT structure determination by DNA sequence analysis.";
RL J. Biol. Chem. 266:3752-3759(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91334397; PubMed-1871117;
RA Huang P.-L., Parks J.E., Rottman W.H., Theologis A.;
RT "Two genes encoding 1-aminocyclopropane-1-carboxylate synthase in
RT zucchini (Cucurbita pepo) are clustered and similar but
RT differentially regulated.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7021-7025(1991).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- INDUCTION: BY WOUNDING IN FRUIT AND ETIOLATED HYPOCOTYLS. BY
CC INDOLEACETIC ACID (IAA)/BENYLADENINE/LICL ONLY IN FRUIT TISSUE.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M58323; AAA33113.1; -
DR EMBL; M61195; AAA33111.1; -

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DR PIR: A38649; A38649.
DR HSP: A41141; A41141.
DR HSP: P37821; 1B86.
DR InterPro: IPR001176; ACC_synthase.
DR Pfan: PF00155; aminotran_1.2; 1.
DR PRINTS: PR00753; ACCSYNTHASE.
DR PROSITE: PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 279 279 PYRIDOXAL PHOSPHATE.
FT CONFLICT 177 177 G -> R (IN REF. 2).
SQ SEQUENCE 493 AA; 55779 MW; 921DC3DFB17A8769 CRC64;

Query Match 64.0%; Score 1637.5; DB 1; Length 493;
Best Local Similarity 63.0%; Pred. No. 8.1e-119;
Matches 312; Conservative 74; Mismatches 96; Indels 13; Gaps 6;

QY 1 MGFKAMDQ--TPLLSKMAGDGHGESSPYFDGWKAYDQNPHTDNPNGVMQGLAENQL 58
Db 1 MGFHQIDERNQALLSKIALDDHGENSAFYDGWKAYDNPFPENPLGVQMGLEAENQL 60
QY 59 TSDLVEDWILNPEASICTPEGINDFRATIANFDYHGLAEFRNAKFAKARTGRNRTFD 118
Db 61 SFDMIVDWIRKHPKPEASICTPEGLERFKSIANFDYHGLPEFRNAIANFMKVRGGRVKFD 120
QY 119 PDRIVMSGGATGAHEVTAFLADPGAEAFVPIPIYPYDGFDRDLRWRTGVKLVPMVCDSSNN 178
Db 121 PSRIYVGGGATGASETIVFCLADPGDAFLVPSYAGDFDRDLKWRTRAGIIRVHCNCSNN 180
QY 179 FVLTKALEDAVEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCD 238
Db 181 FQVTEAALAIYKKAQEAANKVKGVITNPSNPLGTYTORDTLKTLVTFVNHDIHLICD 240
QY 239 EIIYAATVFSQPGFISATIELEDTECDNLVHIVYLSKDMGFGFVRGVIISYNDVAV 298
Db 241 EIIYSATVFKAPTFTSAEIVEQME--HCKKELIHILYLSKDMGLPGFRVGIISYNDVV 298
QY 299 VNCARKMSFGLVSTQTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGGLAKVGIKC 358
Db 299 VRRARQMSFGLVSSQTHLAAMLSDDEVDKFLAENSKRVRGERHARTKELDKMGITC 358
QY 359 LOSNAGLFWMDLRLLKDKQTFKAEMELWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
Db 359 LNSNAGVFWMDLRLLKDKQTFKAEMELWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
QY 419 MDDMAVOIALQIRNFV--LQNK-----VVVSNKKHCWHSNLR--SLKTRRDD--ITMS 469
Db 419 MDDNTVDVALNIHSFVENIDKEDNTVAMPSTKRRHDKNKLSTSFSGRRYDEGNVLNS 478
QY 470 PHSPLQSPMVKATN 484
Db 479 PHTMSPHSLVIAKN 493

RESULT 8
1A12_CUCPE
ID 1A12_CUCPE STANDARD; PRT; 494 AA.
AC Q00379;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase 2 (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACS2 OR ACCLB.
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3663;
RN [1]
RP SEQUENCE FROM N.A.
```

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RX MEDLINE-91334397; PubMed-1871117;
RA Huang P., Parks J.E., Rottman W.H., Theologis A.;
RT "Two genes encoding 1-aminocyclopropane-1-carboxylate synthase in
RT zucchini (Cucurbita pepo) are clustered and similar but
RT differentially regulated.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7021-7025(1991).
CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS
CC MECHANICAL WOUNDING AND A NUMBER OF CHEMICALS.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; M61195; AAA33112.1; -.
DR PIR; B41141; B41141.
DR HSP; P37821; 1B86.
DR Mendel; 247; CUCPE; Accs; 2.
DR InterPro; IPR001176; ACC_synthase.
DR Pfan; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 279 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 345 345 A -> AS (IN REF. 1; AAA33112).
SQ SEQUENCE 494 AA; 55922 MW; 02AE029AA4912C36 CRC64;

Query Match 63.6%; Score 1627.5; DB 1; Length 494;
Best Local Similarity 63.1%; Pred. No. 4.8e-118;
Matches 311; Conservative 73; Mismatches 96; Indels 13; Gaps 6;

QY 1 MGFKAMDQ--TPLLSKMAGDGHGESSPYFDGWKAYDQNPHTDNPNGVMQGLAENQL 58
Db 1 MGFHQIDERNQALLSKIALDDHGENSAFYDGWKAYDNPFPENPLGVQMGLEAENQL 60
QY 59 TSDLVEDWILNPEASICTPEGINDFRATIANFDYHGLAEFRNAKFAKARTGRNRTFD 118
Db 61 SFDMIVDWIRKHPKPEASICTPEGLERFKSIANFDYHGLPEFRNAIANFMKVRGGRVKFD 120
QY 119 PDRIVMSGGATGAHEVTAFLADPGAEAFVPIPIYPYDGFDRDLRWRTGVKLVPMVCDSSNN 178
Db 121 PSRIYVGGGATGASETIVFCLADPGDAFLVPSYAGDFDRDLKWRTRAGIIRVHCNCSNN 180
QY 179 FVLTKALEDAVEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCD 238
Db 181 FQVTEAALAIYKKAQEAANKVKGVITNPSNPLGTYTORDTLKTLVTFVNHDIHLICD 240
QY 239 EIIYAATVFSQPGFISATIELEDTECDNLVHIVYLSKDMGFGFVRGVIISYNDVAV 298
Db 241 EIIYSATVFKAPTFTSAEIVEQME--HCKKELIHILYLSKDMGLPGFRVGIISYNDVV 298
QY 299 VNCARKMSFGLVSTQTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGGLAKVGIKC 358
Db 299 VRRARQMSFGLVSSQTHLAAMLSDDEVDKFLAENSKRVLGERHARTKELDKMGITC 358
QY 359 LOSNAGLFWMDLRLLKDKQTFKAEMELWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
Db 359 LNSNAGVFWMDLRLLKDKQTFKAEMELWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
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Query Match          62.7%   Score 1603.5; DB 1; Length 517;
Best Local Similarity 58.5%; Pred. No. 3.6e-116;
Matches 303; Conservative .80; Mismatches 96; Indels 39; Gaps 5;

Qy      1 MG-FKAMDQTPLLSEKMAIGDGHGSSPYFDGWKKAYDONPFHTDPNGVMQMGLAENOLT 59
|| :|: :||||: |||||: |||||:||:::| | |||:|||||||
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Db	1	MGSYGVYDREILSKIAINDGHGHNUEYFQGWKAYDRDPYHSTKNSGVQIMGLAENQJCL	60
Qy	60	SDLVEDWILANPEASICTPEGINDFRAINFDQYHGLAEFRNAVAFKEMARTGRNRTTFDP	119
Db	61	FDLVTEWLLANPQASICTNEGVNKEMDIAFDQYHGLPEERSAVAFKMGARDEKVIENP	120
Qy	120	DRIVMSGGATGAHEVTAFCLADGCEAPLVPIPIYPYGGFDRDLRWRTGVKLVPMVCDSSNPF	179
Db	121	DRIVMSGGAS-ASETLLFCLANPQDAFLIPSPYYPAFNRDLRWRTGVNLPIPTFCSSSNF	179
Qy	180	VLTKAEALDAYEKAREDNIRVKGLLITNPSPNLGTMDRKTLETVVSEFNKRIHLVCDSE	239
Db	180	KITKEALQSAEYDALKNKIRVKGLVITNPSPNLGTVDLKDTKMLLTFTVNAKNIHLVCDSE	239
Qy	240	IYAATVFSQPFCFISIAEILEDIEDCDRLNHLVHTVSLSKDMGFGPFRVGIIYSYNDVV	299
Db	240	IYATTVNSPFSISVAEVIKMDPHV--NQDLVHLVLSLKDGMGPGFRVGIIYSYNDRV	297
Qy	300	NCAKMSFGVLSTQTOYLLASMLNDDEFVERFLASAKRLAQRFRVFTGGGLAKVGIKCL	359
Db	298	STARMSFGVLSSQTQFMIAALLSDDDFVRRELVLVESRDLFRRHQHTSELAKIGIGCL	357
Qy	360	QSNAGLFVWMDLHOLLKKPTFDSSETELKWKVIIEVKINVSFGYSFHCETPGWFRVCYANM	419
Db	358	QGNALFVWMDLRHLHLDDEATVERELKLRVLIINEVKINVSFGSFLCSEPGWFRVCYANM	417
Qy	420	DDMAVOIALORINFLQNK-----EYVVSNNKKHCWH	451
Db	418	DNATLDVALNIRSFVTRGRVDNSTMTTSARAATTTTTTTTTTTTTTTIKKRGQ	477
Qy	452	SNLRSLKTRFPD-----ITMSPHSPIQPSPMKVA	482
Db	478	MELRSLFNRRFEDGLMSPHSILLSPHSPMPQSPLVKA	515
RESULT	10		
1A14_LYCES			
AC	1A14_LYCES	STANDARD; PRT; 476 AA.	
AC	P29535;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	15-DEC-1998 (Rel. 37, Last annotation update)		
DE	1-aminocyclopropane-1-carboxylate synthase 4 (EC 4.4.1.14) (ACC		
DE	synthase 4) (S-adenosyl-L-methionine methyltransferase-lyase 4)		
DE	(ACS-4).		
GN	ACS4 OR PCVV4B.		
OS	Lycopersicon esculentum (Tomato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
OX	NCBI_TaxID=4081;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-CV. CARUSO; TISSUE-Etiolated hypocotyl;		
RX	MEDLINE=93374928; PubMed=8366090;		
RA	Lincoln J.E., Campbell A.D., Oetiker J., Rottmann W.H., Oeller P.W.,		
RA	Shen N.F., Theologis A.;		
RA	"LE-ACS4, a fruit ripening and wound-induced 1-aminocyclopropane-1-		
FT	carboxylate synthase gene of tomato (Lycopersicon esculentum).		
RT	Expression in Escherichia coli, structural characterization,		
RT	protein characteristics, and phylogenetic analysis.";		
RL	J. Biol. Chem. 268:19422-19430(1993).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Etiolated hypocotyl;		
RX	MEDLINE=92106351; PubMed=1762159;		
RA	Rottmann W.H., Peter G.P., Oeller P.W., Keller J.A., Shen N.F.,		
RA	Nagy B.P., Taylor L.P., Campbell A.D., Theologis A.;		
RT	"1-aminocyclopropane-1-carboxylate synthase in tomato is encoded by a		
RT	multigene family whose transcription is induced during fruit and		
RT	floral senescence.";		
RL	J. Mol. Biol. 222:937-961(1991).		
RL	[3]		

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RP SEQUENCE FROM N.A.
RX MEDLINE=91271385; PubMed=1711229;
RA Olson D.C., White J.A., Edelman L., Harkins R.N., Kende H.;
RT "Differential expression of two genes for L-aminocyclopropane-L-
carboxylate synthase in tomato fruits.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5340-5344(1991).
RN [4]
RP SEQUENCE OF 20-159 FROM N.A.
RC STRAIN=CV. ORLANDO; TISSUE=Fruit;
RX MEDLINE=90280476; PubMed=2191304;
RA van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;
RT "Cloning and sequence of two different cDNAs encoding L-
aminocyclopropane-L-carboxylate synthase in tomato.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:4859-4863(1990).
CC -|- FUNCTION: CATALYZES THE FORMATION OF L-AMINOCYCLOPROPANE-1-
CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine -|- L-
aminocyclopropane-L-carboxylate + methylthioadenosine.
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -|- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -|- SUBUNIT: HOMODIMER.
CC -|- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS
MECHANICAL WOUNDING, A NUMBER OF CHEMICALS AND ANAEROBIOSIS.
CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PROSPHATE-DEPENDENT
AMINOTRANSFERASES.
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CC -----
DR EMBL; M88487; AAA03164.1; -
DR EMBL; X59146; AAA1857.1; -
DR EMBL; M63490; AAA34131.1; -
DR EMBL; M38705; AAA81381.1; -
DR PIR; A40960; A40960.
DR PIR; S19679; S19679.
DR HSP; P37821; I188C.
DR Mendel; 511; LycEs; Acs; 4.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSPEP_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 282 282 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 15 15 V -> A (IN REF. 2).
FT CONFLICT 82 82 T -> A (IN REF. 4).
FT CONFLICT 253 253 S -> P (IN REF. 2).
SQ SEQUENCE 476 AA; 53537 MW; 9BC7D57BD64CB044 CRC64;
Query Match 61.9%; Score 1584; DB 1; Length 476;
Best Local Similarity 65.9%; Pred. NO. 1e-114;
Matches 290; Conservative 72; Mismatches 72; Indels 6; Gaps 2;
QY 11 LLSKMAIGDGHGESSPYDGMKAYDONPHPTDNPNGVMQGLAENOLTSDLVEDWILNN 70
DB 16 VLUSKLAQNEHQENSPYDGMKAYDONDPHVLVNNLNGVQMGLAENOLTSVDLIEEWIKRN 75
QY 71 PEASICTPEGINDFRAINFQDYGHLAEFRNAVAKFMARTGNRTTFQDRIVMSGGATG 130
DB 76 PRASICTNDGIESFRANFQDYGHLPEETNAIAFMETKRGKVKFQAKRVVMAGGATG 135
QY 131 AHEVTAFLADGCEAFPIPIYPYDGFDRDLRWRTQKVLVPVCMDSNNFVLTKEALEADY 190
DB 136 ANETILICLADPGDAFLPPTYPPYGNRDLWRSCVQLLPIPSCKSCNNFKITIEAEAY 195
QY 191 EKAREDNIRVKGLLTNTNSPLGTIMDRKTLTVTVSFINEKRIHLVCDIEYAATVFSQPG 250

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DB 196 EKGOQANVKIKGLIILTNPCNPLGTILDRDTLKKISTFTNEHNIHLVCDIEYAATVFSK 255
QY 251 FTISIAEILEDIEDCDRLNHLVHIVSLKDMGFPGRVCIIVSYNDVAVNCARKWSSFGL 310
DB 256 FVSIATIEIINDNCI--NKDHLHIVSSLKDLGFPGRVGIIVSYNFDDVVVNCARKWSSFGL 313
QY 311 VSTQYLIASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKICLQSNAGLFWMD 370
DB 314 VSTQHLAPLMSDDFEVEELIESAKRLRERYKFTFGLIEIGIKCLESNAGVYCWMD 373
QY 371 LRQLKKPTFQSETELMKVYIHEVKINSPGVSFHCETPGFRVRYANMDDMAVOIALQR 430
DB 374 LRSLLKEATLDAEMSLWKLIIINEVKLNVPSPGSCFSEVGFWRVCFANIDDOTMETALAR 433
QY 431 IRNFV---LQNKVVVSNK 446
DB 434 IRMFMDAYNNVKNKGVMKNK 453
RESULT 11
1A12_ARATH
ID 1A12_ARATH STANDARD; PRT; 496 AA.
AC Q06402;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-aminocyclopropane-2-carboxylate synthase 2 (EC 4.4.1.14) (ACC
synthase 2) [S-adenosyl-L-methionine methylthioadenosine-lyase 2].
GN ACS2 OR ACC1 OR ATL6G1480 OR F22L4.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae;
OC eumetazoa II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=93028584; PubMed=1357670;
RA van der Straeten D., Rodrigues-Pousada R.A., Villarroel R., Hanley S.,
RA Goodman H.M., van Montagu M.;
RT "Cloning, genetic mapping, and expression analysis of an Arabidopsis
thaliana gene that encodes L-aminocyclopropane-L-carboxylate
synthase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9969-9973(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=93066381; PubMed=1438312;
RA Liang X.-W., Abel S., Keller J.A., Shen N.F., Theologis A.;
RT "The L-aminocyclopropane-L-carboxylate synthase gene family of
Arabidopsis thaliana.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11046-11050(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Terry N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.F.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.J., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

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RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT *Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.*;
RL Nature 408:816-820(2000).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = L-
aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- TISSUE SPECIFICITY: HIGH IN DEVELOPING LEAVES AND IN FLOWERS.
CC -1- INDUCTION: BY ETHYLENE.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z12614; CAA78260.1; -;
DR EMBL; M95595; AAB59298.1; -;
DR EMBL; M95594; AAA97516.1; -;
DR EMBL; Y12776; CAA73310.1; -;
DR EMBL; AC061957; AAF81308.1; -;
DR PIR; S31646; S31646.
DR PIR; A47199; A47199.
DR PIR; S46190; S46190.
DR HSSP; P37821; 1B8G.
DR Mendel; 15544; ARATH; Acs.mn15544.
DR InterPro; IPR001176; ACC_synthase.
DR Pfam; PF00155; aminotran_1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Fruit ripening: Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 279 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT VARIANT 136 136 M -> I.
SQ SEQUENCE 496 AA; 55531 MW; 766318AE9B5F1566 CRC64;

Query Match 61.7%; Score 1578; DB 1; Length 496;
Best Local Similarity 59.8%; Pred. No. 3.2e-114;
Matches 297; Conservative 82; Mismatches 102; Indels 16; Gaps 4;

QY 1 MGFRAMDPTLLSKMAYGDGHESSPYDGWKAYDQNPHEPTDNPNGVMQGLAENOLTS 60
DB 1 MGLPGKNGKAVLSKIATNNHGENSEYFDGWKAYDKDPFHLSRNPHGIQMGLEAENQL 60
QY 61 DLVEDWTLNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNITFDPD 120
DB 61 DLKDWKNEPEASICTLEGHQFSDIANFQDYHGLAKKQATIAHFNGKARGGRVTFDPE 120
QY 121 RYVMSGATGAHEVATACLPDGAFLVPYIPYGFDRDLRWRTGVKLVPMVCDSSNFV 180
DB 121 RYVMSGGATGANETIMFCLADPGDVFILPSPYAAAFDRDLRWRTGVIIIPVPCSSDNFK 180
QY 181 LTEALEADAYEKAREDNIRYKGLLITNPSNPLGTIMDKTLRTVVSFINKEIHLVDEI 240
DB 181 LTVDAEAWYAKKAGESNKKVGLLITNPSNPLGTIMDKTLRTVVSFINKEIHLVDEI 240
QY 241 YAATVSPQPGFISTAEILEDETIEDCRNLVHIYISLSKDMGFGFRGVGIYSYNDVAVN 300
DB 241 YAATVSPQPGFISTAEILEDETIEDCRNLVHIYISLSKDMGFGFRGVGIYSYNDVAVN 300
DB 241 YAATVSPQPGFISTAEILEDETIEDCRNLVHIYISLSKDMGFGFRGVGIYSYNDVAVN 300

QY 301 CARMSFGLVSTQVYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGGLAKVGIKQLQ 360
DB 301 CARMSFGLVSSQTLMLASMLSDQFVDFNLFMESSRLGIRHKVFTTGTKKADIACLT 360
QY 361 SNAGLFVWMDLRQLLK-KPTFDSSETLWKVLIIEHVKNVSPGYFHCCTEPCGFRVCYANM 419
DB 361 SNAGLFVWMDLRQLLK-KPTFDSSETLWKVLIIEHVKNVSPGYFHCCTEPCGFRVCYANM 420
QY 420 DDMVAQIALQIRNFVLQNKVVV-----SNKKHW-HSNLRSLKTRRDEDD 465
DB 421 DDDTLHVALGRIQDFSVSKNKNIVEKASENDQVIONKSARKLKWOTQNLRLSFR-RLYED 479
QY 466 ITMSPHSPPLQSPMVA 482
DB 480 GLSSPGIMSPHSPPLRA 496

RESULT 12

1A1C_MALDO STANDARD; PRT; 473 AA.
ID 1A1C_MALDO STANDARD; PRT; 473 AA.
AC P37821; Q40278; O04993;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC
synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACS-1.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. GOLDEN DELICIOUS; TISSUE=Fruit cortical tissue;
RX MEDLINE=95232185; PubMed=7716231;
RA Lay-Yee M., Knighton M.L.;
RT "A full-length cDNA encoding 1-aminocyclopropane-1-carboxylate
synthase from apple."
RL Plant Physiol. 107:1017-1018(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. GOLDEN DELICIOUS;
RA Harada T., Sunako T., Sakuraba W., Goto S., Senda M., Akada S.,
RA Ishikawa R., Niizeki M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 10-473 FROM N.A.
RC STRAIN-CV. GOLDEN DELICIOUS; TISSUE=Fruit;
RA Dong J.G., Kim W.T., Yip W.K., Thompson G.A., Li L., Bennett A.B.,
RA Yang S.F.;
RT "Cloning of a cDNA encoding 1-aminocyclopropane-1-carboxylate synthase
and expression of its mRNA in ripening apple fruit."
RL Planta 185:38-45(1991).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.37 ANGSTROMS).
RX MEDLINE=20079531; PubMed=10610793;
RA Capitani G., Hohenester E., Feng L., Storici P., Kirsch J.F.,
RA Jansonius J.N.;
RT "Structure of 1-aminocyclopropane-1-carboxylate synthase, a key
enzyme in the biosynthesis of the plant hormone ethylene."
RL J. Mol. Biol. 294:745-756(1999).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = L-
aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
CC -----

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DR EMBL; L31347; AAA73941.1; -;
DR EMBL; U09156; AAB68617.1; -;
DR EMBL; U03294; AAA03472.1; -;
DR PDB; 1B8G; 26-JAN-00.
DR Mendel; 251; Maldo; Acs:1.
DR Mendel; 9005; Maldo; Acs:2.
DR InterPro; IPR001176; ACC_synthase.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
FT Multigene family; 3D-structure.
FT BINDING 273 273 PYRIDOXAL PHOSPHATE.
FT CONFLICT 15 15 Q -> E (IN REF. 3).
FT CONFLICT 101 101 E -> K (IN REF. 3).
SQ SEQUENCE 473 AA; 53250 MW; 6ACA20759615E75D CRC64;

Query Match 52.4%; Score 1341; DB 1; Length 473;
Best Local Similarity 53.0%; Pred. No. 5,6e-96;
Matches 251; Conservative 83; Mismatches 126; Indels 14; Gaps 5;

QY 11 LLSKMAIGDHGESSPYFDGWKAYQONPHPTDNPNGVMQGLAENQLTSLDVEDWILNN 70
DB 3 MLSRNTNSHGQDSYFLGWEYKPNYHEVHTNPNGIOMGLAENQLCFLLESWLAKN 62
QY 71 PEASICTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNITRTPDRIVMSGGATG 130
DB 63 PAAAFKNGESIFAEALFQDYGHLPAFKKAWDFMAEIRGNKVTFDPNHLVLTAGATS 122
QY 131 AHEVTAFLADPGAEFLVPIYPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 190
DB 123 ANETFLCLAEAGDAFLPTYPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 182
QY 191 EKAREDNTRVGLLTNPSNPLGTTMDRKTLTIVVSYFNEKRIHLVDEIYAATVFSQPG 250
DB 183 QBAERNLRVKGLVITNPSNPLGTTMTNRELYLLSFEVDKGIHLISDEIYSGTAFSSPS 242
QY 251 FTISAEILEDETDIEDCRN-----LVHIVYSLSKDMGPPRVRGVIYSYNDVAVNCARKM 305
DB 243 FTSVMEVLKDR---NCDENSEVQVRVYVYSLKDLGLGFRVGAISYNDVAVNAATKM 299
QY 306 SSFGLVSTQTOYLLASMLNDDSEVRFVLAESAKRLAQRFRVFTGGKLVKIGKCLQSNAGL 365
DB 300 SSFGLVSSQTHLLSAMLSDKLTKNYTAENHKRLQKQKLVSLGSLQSGISCLNGNAGL 359
QY 366 FVWMDLRQLLKPTFDSSETELWKVVIHEWKNVSPGYSEFHCTEPGRVFCVYANMDMAVQ 425
DB 360 FCWDMRHLRLSTFAEMELMKKIVYEVHLNISPSSCHCTEPCGWFRCVCFANLPERTID 419
QY 426 IALQIRIRNFVLQNKVWV----SNKKHCWHSNLRSLKLTTRDDTDTMSPHSPLP 475
DB 420 LAMQRLKAFVGYVYVPEVNGSQSSHLHSR-RQSL-TKKVSRSLSFDDRGDIP 471

RESULT 13
ID 1A12_CUCMA STANDARD; PRT; 475 AA.
AC Q00257;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase CMA101 (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).

GN ACS2 OR PCVAA.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Erosoidae; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RP SEQUENCE FROM N.A.
RP RA Nakagawa N., Mori H., Yamazaki K., Imaseki H.;
RT "Cloning of a complementary DNA for auxin-induced 1-aminocyclopropane-1-carboxylate synthase and differential expression of the gene by auxin and wounding.";
RL Plant Cell Physiol. 32:1153-1163(1991).
RP SEQUENCE FROM N.A.
RP RA Nakagawa N., Kamiya Y., Imaseki H.;
RT "Nucleotide sequence of an auxin-regulated 1-aminocyclopropane-1-carboxylic acid synthase gene from Cucurbita maxima Duch.";
RL (In) Plant Gene Register PGR95-110.
CC -|- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine -|- 1-aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -|- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -|- SUBUNIT: HOMODIMER.
CC -|- INDUCTION: BY TISSUE WOUNDING AND AUXIN.
CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

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DR EMBL; U37774; AAA91152.1; -;
DR EMBL; D01033; BAA00839.1; -;
DR PIR; JQ2214; JQ2214.
DR HSSP; P37821; 1B8G.
DR Mendel; 245; CUCma; Acs:2.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 272 272 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 475 AA; 53481 MW; D02A666E137F44A0 CRC64;
Query Match 52.3%; Score 1339.5; DB 1; Length 475;
Best Local Similarity 55.3%; Pred. No. 7.3e-96;
Matches 246; Conservative 84; Mismatches 110; Indels 5; Gaps 3;
QY 11 LLSKMAIGDHGESSPYFDGWKAYQONPHPTDNPNGVMQGLAENQLTSLDVEDWILNN 70
DB 3 MLSRNTNSHGQDSYFLGWEYKPNYHEVHTNPNGIOMGLAENQLCFLLESWLAKN 62
QY 71 PEASICTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNITRTPDRIVMSGGATG 130
DB 63 PDAASFKRDKGSIFRELALFQDYGHLPAFKKALVEFMAEIRGNKVSYFEANNVLTAGATS 122
QY 131 AHEVTAFLADPGAEFLVPIYPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 190
DB 123 ANETFLCLAEAGDAFLPTYPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 182
QY 191 EKAREDNTRVGLLTNPSNPLGTTMDRKTLTIVVSYFNEKRIHLVDEIYAATVFSQPG 250
DB 183 KDAQTRNLRVKGLVITNPSNPLGTTMTNRELYLLSFEVDKGIHLISDEIYSGTAFSSPS 242

QY 251 FTISIAILEDIT--DIECDNLVHIVYSLSKOMGPFPGFRVGIYSYNDVAVNCARKMSF 308
Db 243 FVSAMEVLKERSSEDEWKR-VHIVYSLSKDGLGFRVGIYSYNDVAVNCARKMSF 301
QY 309 GLVSTQVYLLASMLNDDEFVERFLAESAKRLAQFRVFTGGGLAKVGIKQCSNAGLFW 368
Db 302 GLVSSQVYLLASMLNDKFTTSYISENKRQKQKMLVSGLOKAGINCSDNAGLFCW 361
QY 369 MDLRQLKKPTDSETELKWKIIVHEVKINVSPOYSHCHTEPGFRVCIYVAVMDMAVOIAL 428
Db 362 VDMRHLLSDKFESELELWKIVYVGLNISPSSCHCTEPGFRVCFANMSESTLKAV 421
QY 429 QRLNFEVLQNKVYVSNKKCHHSN 453
Db 422 RLKSFVTELRSTTSNHRN--HDN 444

RESULT 14
LALL_ORYSA STANDARD; PRT: 487 AA.
ID LALL_ORYSA
AC Q07215;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC
synthase 1) (S-adenosyl-L-methionine methylthioadenosine-lyase 1).
GN ACC1.
OS *Oryza sativa* (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; *Oryza*.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93283732; PubMed=8389618;
RT Zarembinski T.I., Theologis A.;
RT "Anaerobiosis and plant growth hormones induce two genes encoding 1-
aminocyclopropane-1-carboxylate synthase in rice (*Oryza sativa* L.).";
RL Mol. Biol. Cell 4:363-373(1993).
CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- INDUCTION: BY ANAEROBIOSIS AND INDOLACETIC ACID (IAA) +
BENZYLADENINE (BA) + LICI TREATMENT.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL: M96672; AAA33887.1; -;
DR EMBL: M96673; AAA33888.1; -;
DR HSP: P37821; I886.
DR InterPro: IPR001176; ACC_synthase.
DR InterPro: IPR001511; Aminotran_1.
DR Pfam: PF00155; aminotran_1.2; 1.
DR PRINTS: PR00753; ACCSYNTHASE.
DR PROSITE: PS00105; AA_TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
Multigene family.
FT BINDING 286 286 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT VARIANT 129 129 N -> T.
FT VARIANT 151 151 F -> L.

FT VARIANT 273 273 G -> D.
SQ SEQUENCE 487 AA; 53101 MW; 90FB80DEF3524009 CRC64;

Query Match 49.2%; Score 1258.5; DB 1; Length 487;
Best Local Similarity 53.9%; Pred. No. 1.3e-89;
Matches 236; Conservative 77; Mismatches 116; Indels 9; Gaps 4;

QY 5 AMDOTPLLSKMAIGDGHGSSPYFDGWKAYDQNPFFHTDNPNGVMQGLAENQITSLVE 64
Db 7 AEEKPOLLSSKAGCNSHGDSYFLGWQYEKNPFDVSNPSTGIOMGLAENQLSFDLLE 66

QY 65 DWILNNEPASICPE--GINDERAIAFNODYHGLAEFRANAVAKFMARTGRIITFDORI 122
Db 67 EWLEKNPHALGLRREGGASVRELALFDYHGLPAEKNALARFMSQRGYKVVFDPSNI 126

QY 123 VMSGATGAHEVTAFCIADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMCDSSNNFVLT 182
Db 127 VLNAGATSANEALMFCIADHGAFFIPTPYPGFDRDLKWRGAEIVPVHCASANGFRVT 186

QY 183 KEALDAYEKAREDNIRVKGLITNPSPNPLGTINDRKTLTFTVVSFINNEKRIHLVCEIYA 242
Db 187 RAALDDAYRAQRRRLRVKGLITNPSPNPLGTASPRADLETIVDFVAAKGTHLISDEIYA 246

QY 243 ATVFSOP--GFISTAEILEDETDIEC--DRNLVHIVYSLSKOMGPFPGFRVGIYSYNDA 297
Db 247 GTFAEPAGVSALEVVAGRDGGGAGVSDR--VHVYSLSKDGLGFRVGIYSAANAA 304

QY 298 VVNCARKMSFGLVSTQVYLLASMLNDDEFVERFLAESAKRLAQFRVFTGGGLAKVGIK 357
Db 305 VVSAATKMSFGLVSSQVYLLAALLGDRDFTSRVVAENKRRIKERHDQLVDGLREIGIG 364

QY 358 CLOSAGLFWMDLRQLKKPTDSETELKWKIIVHEVKINVSPOYSHCHTEPGFRVCIYA 417
Db 365 CLFSNAGLFCWVDMSHLMRSRSEFAGELMKVYVFEVGLNISPSSCHCTEPGFRVCF 424

QY 418 NMDDMAVOIALQRLNFEV 435
Db 425 NMSAKTLDVAMQRLRSFV 442

RESULT 15
AAT_AQUAE STANDARD; PRT: 394 AA.
ID AAT_AQUAE
AC Q67781;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPAT).
GN ASPC OR AQ_1969.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aufay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus".
RL Nature 392:353-358(1998).
CC -!- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +
L-glutamate.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.

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Query Match	73.3%	Score 1875.5;	DB 2;	Length 490;
Best Local Similarity	71.9%;	Pred. No. 5e-200;		
Matches 348; Conservative 68; Mismatches 59; Indels 9; Gaps 6;				
QY	7	DQTPLLSKMAIGDGHGSSPYFDGWKAYDNPPHPTDNPNGVMQGLAENOLTSDLYEDW	66	
	:	: : : :		
Db	9	NQRTLLSKMATGCHGENSPYFDGWKAYDNNPFLTQNPGVIOMGLAENQLSFELIEQW	68	
	:	: : : :		
QY	67	ILANPEASICTPEGINDFRAIANFQDYHGIAEFNAVAKMARTRGNRRITFPDPRIYMSG	126	
	:	: : : :		

Db 69 VLNNPQASICTAGQLQEFKDTAIFQDYHGLQSSDMLFANFMGKVRGNRVTFNDPDRIVMSG 128
QY 127 GATGAHEVTAFCADPGEAFVPIPIYPGCFDRDLRWRTGVKLVLP-VMCDSSNNFVLTKREA 185
Db 129 GATGAHEMTAFCLADPGDAFLVPTYPYPGCFDRDLRWRTGVQIPVVVCESENFRITRSA 188
QY 186 LEDAYEKAREDIRYKGLLITNPSNPLGTIMDRKTLRTVVSFINBKRIHLVCDIYAATV 245
Db 189 LBEAVERAQEDKIRYKGLLITNPSNPLGTILDRETLVSLVSPINEKNIHLVCDIYAATV 248
QY 246 FSQPGFISIAETLEDETDCDRNLVHIVYSLSKDMPGPFVGVIIYSYNDVAVNCARKM 305
Db 249 FSQPAFVSAEYIEQE-NVSCNRDLHIHIVYSLSKDMPGPFVGVIIYSYNDVAVNCARKM 307
QY 306 SSGFLVSTQTYLLASMLNDFEVRFLAESAKRLAQFRVFTGGLAKVGIKCLOSNAGL 365
Db 308 SSGFLVSTQTYLLASMLNDFEVRFLAESAKRLARRYTTTTRGLAQVNICLSNGGL 367
QY 366 FVMDLRQLLKKPTDSETELWKVIHEVKINVSFGYFHCTEPGWFRVCYANMDDMAVQ 425
Db 368 FIWMDLRLLKKEKTEAEAMLRVINEVKLVNVPASPHCSEPGWFRVCYANMDDMTMQ 427
QY 426 IALORIRNVLQNKVVV--SNKKCHWSNL-RLSLKTRRFDIT--MSPHSPLPQSPM 479
Db 428 VALRIITFALQNKAAVLPALIKROCWMONLRLSLSRFRDFTMSPMSPHSP1-QSPL 486
QY 480 VKAT 483
Db 487 VRAT 490

RESULT 2
US-08-485-107-2
; Sequence 2, Application US/08485107
; Patent No. 5767376
; GENERAL INFORMATION:
; APPLICANT: STILES, JOHN I.
; APPLICANT: NEUPANE, KABI R.
; TITLE OF INVENTION: ACC SYNTHASE GENE AND ITS USE IN PLANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAVERTOCK, MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,107
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UH-01170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8310
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-107-2

Query Match 71.2%; Score 1823; DB 1; Length 487;

Best Local Similarity 70.9%; Pred. No. 3.5e-194;
Matches 339; Conservative 65; Mismatches 66; Indels 8; Gaps 3;
QY 11 LLSKMAIGDGHGCHESPPYFDGWKAYQONPPHPTDNDNGVQMGLAENQLTSLDVLVDWILNN 70
Db 10 LLSKIAT:NGHGEDSPYFDGWKAYSDPDPHPTQNPPEGVIQMGLAENQLCFNLHIEWLLKN 69
QY 71 PEASICTPEGINDFRAIANFQDYHGLAEPNNAVAKFMAKTRNRTITFDPRIVMSGGATG 130
Db 70 PEASICTAGAAEFEDIAIFQDYHGLAEREAVAKFMGKVRNRASFFDPRIVMSGGATG 129
QY 131 AHEVTAFCADPGEAFVPIPIYPGCFDRDLRWRTGVKLVPMCDSSNNFVLTKREALEDAY 190
Db 130 AHEMTAFCLADPGDAFLVPTYPYPGCFDRDLRWRTGVQIPVVVCESENFRITSAEAA 189
QY 191 EKAREDIRYKGLLITNPSNPLGTIMDRKTLRTVVSFINBKRIHLVCDIYAATVFSQPG 250
Db 190 ETAQEDAKIKVGLLITNPSNPLGTITITDLEALVFTTNHKNHLVCDIYAATVFSQPE 249
QY 251 FTSIAEILEDDETDIECDRLVHIVYSLSKDMPGPFVGVIIYSYNDVAVNCARKMSSFG 310
Db 250 FTSIAEIE-EDKICNRDLHIHIVYSLSKDMPGPFVGVIIYSYNDVAVNCARKMSSFG 308
QY 311 VSTQTYLLASMLNDFEVRFLAESAKRLAORFVFTGGLAKVGIKCLOSNAGLVFVMD 370
Db 309 VSSQTYLLASMLADFEVDQFIVESKRLAMRHSFFFTQRLAQVINGICLSNAGLVFVMD 368
QY 371 LRQLLKKPTDSETELWKVIHEVKINVSFGYFHCTEPGWFRVCYANMDDMAVOIALOR 430
Db 369 LRRLKEQTFEAMVLRVINEIKLVNVPASPHCSEPGWFRVCYANMDDMTMETALS 428
QY 431 IRNFVLQNKVVVSNKKCHWSNLRLSLKTRRFDIT-----MSPHSPLPQSPMVK 482
Db 429 IKTEMLQHKAEAMVPKKLQWQTSRLSLFSS-RYEDIMETPGSFMSPHSP1QSPPLVRA 485
RESULT 3
US-08-378-313-31
; Sequence 31, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-378-313-31

Query Match 69.2%; Score 1771.5; DB 4; Length 483;
Best Local Similarity 68.9%; Pred. No. 1.9e-188;
Matches 326; Conservative 76; Mismatches 66; Indels 5; Gaps 3;

QY 11 LLSKMATGDCGESSPYFDGKAWQNPHTDNPNGVMQGLAENOLTSVLVEDWLN 70
DB 13 LLSKIATNDGHEGSPYFDGKAWNPHTDNPNGVMQGLAENOLTSVLVEDWLN 72

QY 71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNRTDPPDRIVMSGGATG 130
DB 73 PKASICTVEGAENFDIAIFQDYHGLPEFRQAVARFMEKVRGDRVTFDPNRIVMSGGATG 132

QY 131 AHEVTAFCCLADPGAFVLPYYPGFDRLNRWRTGKLVPMCDSSNNFVLTKALEDAY 190
DB 133 AHEMLAFCCLADPGAFVLPYYPGFDRLNRWRTGKLVPMCDSSNNFVLTKALEEAY 192

QY 191 EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDIYAATVFSQP 250
DB 193 EKAQSNIRKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDIYAATVFSQP 252

QY 251 FISTAEILEDETDIECDNRNLVHIYVSLSKDMGPFGRVGIYVSYNDVAVNCARKMSFGL 310
DB 253 FISVSENVEM--TECTDLHIYVSLSKDLGPFGRVGIYVSYNDVAVNCARKMSFGL 310

QY 311 VSTOTQYLLASMLNDDFEVERFLAESAARLAQRVFTGGLAKYGIKCLQSNAGLFFVMD 370
DB 311 VSTOTQYLLASMLNDDFEVERFLAESAARLAQRVFTGGLAKYGIKCLQSNAGLFFVMD 370

QY 371 LRQLLKPTDSETELAQVITHEVKINVSFCYSPHCPEGWFRVVCYANMDDMAVOIALOR 430
DB 371 LRQLLKPTDSETELAQVITHEVKINVSFCYSPHCPEGWFRVVCYANMDDMAVOIALOR 430

QY 431 IRNFVLQKNEY--YVSNKKHCWHNSLNKTRFRDDITMSPHSPLPQSPMAVK 481
DB 431 IRNFVLQKNEY--YVSNKKHCWHNSLNKTRFRDDITMSPHSPLPQSPMAVK 482

RESULT 4
US-08-695-412B-10
; Sequence 10, Application US/08695412B
; Patent No. 5874269
; GENERAL INFORMATION:
; APPLICANT: STILES, JOHN I.
; APPLICANT: MOISYADI, STEFAN
; APPLICANT: NEUPANE, KABI R.
; TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
; TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
; TITLE OF INVENTION: RIPENING OF COFFEE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JONES, DAY, REAVIS & POGUE
; STREET: NORTH POINT, 901 LAKESIDE AVENUE
; CITY: CLEVELAND
; STATE: OHIO
; COUNTRY: USA
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS v. 5.1
; SOFTWARE: WordPerfect v. 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,412B

; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/485,107
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRIFFITH, CALVIN P.
; REGISTRATION NUMBER: 34,831
; REFERENCE/DOCKET NUMBER: 265036600002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 586-7050
; TELEFAX: (216) 579-0212
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 488 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1653
; US-08-695-412B-10

Query Match 69.1%; Score 1768; DB 2; Length 488;
Best Local Similarity 67.1%; Pred. No. 4.8e-188;
Matches 325; Conservative 83; Mismatches 66; Indels 10; Gaps 5;

QY 7 DOTLLSKMATGDCGESSPYFDGKAWQNPHTDNPNGVMQGLAENOLTSVLVEDW 66
DB 8 EQOQLLSKMATNDGHEGSPYFDGKAWQNPHTDNPNGVMQGLAENOLTSVLVEDW 67

QY 67 ILNNEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNRTDPPDRIVMSG 126
DB 68 VLNNEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNRTDPPDRIVMSG 127

QY 127 GATCAHEVTAFCCLADPGAFVLPYYPGFDRLNRWRTGKLVPMCDSSNNFVLTKALE 186
DB 128 GATCAHEVTAFCCLADPGAFVLPYYPGFDRLNRWRTGKLVPMCDSSNNFVLTKALE 187

QY 187 EDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDIYAATV 246
DB 188 EAYAKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDIYAATV 247

QY 247 SQPGFISIAEILEDETDIECDNRNLVHIYVSLSKDMGPFGRVGIYVSYNDVAVNCARKMS 306
DB 248 SQPGFISIAEILEDETDIECDNRNLVHIYVSLSKDMGPFGRVGIYVSYNDVAVNCARKMS 305

QY 307 SFGVSVTQYLLASMLNDDFEVERFLAESAARLAQRVFTGGLAKYGIKCLQSNAGL 366
DB 306 SFGVSVTQYLLASMLNDDFEVERFLAESAARLAQRVFTGGLAKYGIKCLQSNAGL 365

QY 367 VMMDLRQLLKPTDSETELAQVITHEVKINVSFCYSPHCPEGWFRVVCYANMDDMAVOI 426
DB 366 FMDLRQLLKPTDSETELAQVITHEVKINVSFCYSPHCPEGWFRVVCYANMDDMAVOI 425

QY 427 ALQIRNFVL-QNKEY-VVSNKKHCWHNSLNKTRFRDDITMSPHSPLPQSPM 479
DB 426 ALQIRNFVL-QNKEY-VVSNKKHCWHNSLNKTRFRDDITMSPHSPLPQSPM 478

QY 480 VKAT 483
DB 485 VRAT 488

RESULT 5
US-08-378-313-30
; Sequence 30, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO

; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-378-313-30

Query Match 68.6%; Score 1755.5; DB 4; Length 485;
Best Local Similarity 68.8%; Pred. No. 1.2e-186;
Matches 327; Conservative 76; Mismatches 65; Indels 7; Gaps 5;

QY 11 LLSKNAIGDGHGESSPYFGWKAYDONPHPTDNPNGVMQGLAENQLTSDLVEDWILNN 70
DB 13 LLSKATNDGHSNSPYFGWKAYANNPHLTDNPTGTQMGLEAENQLCFDLIQEWVNN 72
QY 71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAFKFMARTGNRITFDPDRIVMSSGATG 130
DB 73 PRASICTVEGAENFQDIAFQDIHGLPEFRQAVAFKFMKVRGDRVTFDNPRIVMSSGATG 132
QY 131 AHEVTAFCIADPGAEFLVPPIYPYPGFDRDLRWRTGVKLVPMCDSSNNFVLTKAELEDAY 190
DB 133 AHEMLAFCLADPGDAFLVPTPIYPYPGFDRDLRWRTGVQLFPVVCESNDKFKVTTKALEEAY 192
QY 191 EKAREDNIRKGLLTNPSPNGTMDRKTLTVTVSFINEKRIHLVCDBIYAATVFSQPG 250
DB 193 ERAQOOSNIKIGLLINPNPGLTLDKTDLRDITVFINSKNIHLVCDBIYAATVFDQPG 252
QY 251 FTISIAELEDETDIECDRLNHLVIVSLSKDMGFPGRVGIYISYNDVAVNCARKMSSEGL 310
DB 253 FLSVSEIVEDM--IECNKDLIHIVISLSDKLGFPGRVGIYISYNDVAVNCARKMSSEGL 310
QY 311 VSTQTOYLLASLNDDEFVERELAESAQLAQRFRVFTGGLAKVGTICKLQSNAGLFVWMD 370
DB 311 VSTQTOHLLASLSDRVFDKFAESSERLGERQGMFTKGLAEVIGSLKSNAGLFFWMD 370
QY 371 LRQLLKKPTFDESETELWKVIIIEVKINVSFSGFCHCTPGFGRVVCYANMMDMAVIALQR 430
DB 371 LRRLLEATFDESELELWRIIIEVKINVSFSGFCHCTPGFGRVVCYANMMDTMRIALKR 430
QY 431 IRNFVLQNKREV--VVSNNKHKCHWSNLRLSLKTRRFD-DITMSP-HSPLOSMPVK 481

DB 431 ISYFVLQPKGLNNIAAIKKQCSRRKLQISLSFRRLDHEFMNSPAHSPM-NSPLVR 484
RESULT 6
US-08-378-313-27
; Sequence 27, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-313-27

Query Match 66.9%; Score 1713; DB 4; Length 485;
Best Local Similarity 65.6%; Pred. No. 6.4e-182;
Matches 319; Conservative 72; Mismatches 89; Indels 6; Gaps 4;

QY 1 MGFKAMDQTPLLSKNAIGDGHGESSPYFGWKAYDONPHPTDNPNGVMQGLAENQLT 60
DB 1 MGFETAKTNSIISLKLATNEEHGNSPYFGWKAYSDPFPHLKPNPVGVIQMGLEAENQLCL 60
QY 61 DLVEDWILNPNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAFKFMARTGNRITFDPD 120
DB 61 DLIEDWIKRNPKGSTCS-EGIKSFKAIANFQDYHGLPEFRKAIAKFMKTRGRVRFDE 119
QY 121 RIVMSGGATGAHEVTAFCIADPGAEFLVPPIYPYPGFDRDLRWRTGVKLVPMCDSSNNFV 180
DB 120 RYVMAGGATGANETIIFCLADPGDAFLVPSPYPAPFNRLRWRTGVQLPIHCSSNNFK 179
QY 181 LTKAELEDEYKAREDNIRKGLLTNPSPNGTMDRKTLTVTVSFINEKRIHLVCDBI 240
DB 180 IISKVAYENAEYNAQSNIRKGLLTNPSPNGTMDRKTLTVTVSFINEKRIHLVCDBI 239
QY 241 YAATVFSQPGFISIAELEDETDIECDRLNHLVIVISLSDKMGFPGRVGIYISYNDVAVN 300
DB 240 YAATVFTDTPQFVSIAELEDEQWNTCYCNKDLHIVISLSDKMGFLPGRVGIYISFNDDVN 299

;; APPLICANT: SATO, TAKAHIDO
;; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
;; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,313
;; FILING DATE:
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/862,493
;; FILING DATE: 02-APR-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MURASHIGE, KATE H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 29190-20002.20
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 856-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 493 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-378-313-21

Query Match 64.0%; Score 1636.5; DB 4; Length 493;
Best Local Similarity 63.0%; Pred. No. 2.2e-173;
Matches 312; Conservative 74; Mismatches 96; Indels 13; Gaps 6;
QY 1 MGFKAMDQ--TPLLSKMAIGDGHGSSPYFDGWKAYDQNPHTDNPNGVMQGLAENOL 58
DB 1 MGFHQIDERNQALLSKIALDDHGENSPYFDGWKAYDNDPFHPENNPLGVQMGLAENOL 60
QY 59 TSDLVEDWILNNPEASICTPEGINDFRATIANFDYHGLAEFRNAVAKFMARTGRNRTFD 118
DB 61 SFDMIVDWIRKHPKPEASICTPEGLERFKSIANFDYHGLPEFRNAIANFMGKVRGGRVKPD 120
QY 119 PDRIVMSGGATGAHEVTAFCPLADPGAEAFVPIYPYPGFDRDLRWTGKVLVPMCDSSNN 178
DB 121 PSRIVGGGATGASETIVFCLADPGDAFLVPSPYAGDFDLKWRTRAQIIRVHCNRSNN 180
QY 179 FVLTKEADEAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCD 238
DB 181 FQVTKAALEIAYKKAQEAENKVKGLIITNPSNPLGTITDRTDLTKLTVFVNHDLICD 240
QY 239 ELYAATVVSQPCFISATLEDETIEDCORNLVHIVSLSKDMGPPGFRVGLIISYNDAY 298
DB 241 ELYSATVFKAPFTTSIAEIVEQME--HCKKELIHLIYLSKDMGLPGFRVGLIISYNDVY 298
QY 299 VNCARMSFGLVSTQTYLLASMLNDDFVERFLAEAKRLAQRFRTVGTGLAKVGKIC 358
DB 299 VRRARQMSFGLVSSQTHLAAMLSDDEPDVDFLAENSKRVGERHARETKELDKWGTC 358
QY 359 LOSNAGLFVMDLROLLKPTFDESETELMKVIHEVKNVSPGYSFHCTEPGWFRVCYAN 418
DB 359 LNSNAGVFMMDLRLLDQTEKAEMLWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
QY 419 MDDMAVOIALQIRNFV--LQNK---VVVSNKKHCWHSNLR--SLKTRRDE--ITMS 469

DB 419 MDDNTVDVALNRIHSFVENIDKEDNTVAMPSTRHRONKLRLSFSFGRRYDEGNVLNS 478
QY 470 PHSPLPQSPVMKATN 484
DB 479 PHTMSPHSPPLVIKN 493
RESULT 13
US-08-378-313-28
;; Sequence 28, Application US/08378313
;; Patent No. 6207881
;; GENERAL INFORMATION:
;; APPLICANT: THEOLOGIS, ATHANASIOS
;; APPLICANT: SATO, TAKAHIDO
;; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
;; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 Page Mill Road
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,313
;; FILING DATE:
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/862,493
;; FILING DATE: 02-APR-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MURASHIGE, KATE H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 29190-20002.20
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 856-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 493 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-378-313-28

Query Match 64.0%; Score 1636.5; DB 4; Length 493;
Best Local Similarity 63.0%; Pred. No. 2.2e-173;
Matches 312; Conservative 74; Mismatches 96; Indels 13; Gaps 6;
QY 1 MGFKAMDQ--TPLLSKMAIGDGHGSSPYFDGWKAYDQNPHTDNPNGVMQGLAENOL 58
DB 1 MGFHQIDERNQALLSKIALDDHGENSPYFDGWKAYDNDPFHPENNPLGVQMGLAENOL 60
QY 59 TSDLVEDWILNNPEASICTPEGINDFRATIANFDYHGLAEFRNAVAKFMARTGRNRTFD 118
DB 61 SFDMIVDWIRKHPKPEASICTPEGLERFKSIANFDYHGLPEFRNAIANFMGKVRGGRVKPD 120
QY 119 PDRIVMSGGATGAHEVTAFCPLADPGAEAFVPIYPYPGFDRDLRWTGKVLVPMCDSSNN 178
DB 121 PSRIVGGGATGASETIVFCLADPGDAFLVPSPYAGDFDLKWRTRAQIIRVHCNRSNN 180
QY 179 FVLTKEADEAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCD 238
DB 181 FQVTKAALEIAYKKAQEAENKVKGLIITNPSNPLGTITDRTDLTKLTVFVNHDLICD 240

QY	239	EIYAATVFSOPGISIAEILEDTECDRLNVHVIYSLSKDWGFFGFRRVGIISYNDAV	299
		: :	
Db	241	EIYATVFRAPTSTAEIVQE--HCKELIHILYSLSKDWGLPGFRVGIIYSYNDAV	298
-QY	299	VNCARWSSFLYSTOTVYLASMLNDDEVERELAESAQRLAQRVFTTGGIAKVGIKC	358
		: : : : : : :	
Db	299	VRARQMSSFGLVSSQTQLLAAMLSDDFDKFLAENSKRVRERHARETKELDKMGITC	358
QY	359	LQSNAGLFWMDLRQLKKPTFDSFTELWKVIIHEVKINVSFCYSPHCWTFEGWFRVCYAN	418
		: : : : : : :	
Db	359	LNSNAGVFWMDLRLLLKDTQFAEMELRWIINEVKLVNPSGSSEHVHTPEGWFRVCVAN	418
QY	419	MDDMAVOIALQRTNFV--LONKE---VVVSNKKHCWHSNLRI--SLKTRRDD--ITMS	469
		: : : : : : : :	
Db	419	MDDTVDALNRTHSFVENIDKEDNTVAMPSKTRHRDNKLRLSFSFGRRYDEGNVLNS	478
QY	470	PHSPQPSPMKATN 484	
		: : :	
Db	479	PHTMSPHSPLVIAKN 493	
		: : :	
RESULT 14			
US-08-378-313-23			
; Sequence 23, Application US/08378313			
; Patent No. 6207881			
; GENERAL INFORMATION:			
; APPLICANT: THEOLOGIS, ATHANASIOS			
; APPLICANT: SATO, TAKAHIDO			
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH			
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS			
; NUMBER OF SEQUENCES: 34			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: MORRISON & FOERSTER			
; STREET: 755 Page Mill Road			
; CITY: Palo Alto			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94304-1018			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/378,313			
; FILING DATE:			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/862,493			
; FILING DATE: 02-APR-1992			
; ATTORNEY/AGENT INFORMATION:			
; NAME: MURASHIGE, KATE H.			
; REGISTRATION NUMBER: 29,959			
; REFERENCE/DOCKET NUMBER: 29190-20002.20			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 856-5600			
; TELEFAX: (415) 494-0792			
; TELEX: 706141			
; INFORMATION FOR SEQ ID NO: 23:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 494 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-378-313-23			

Query Match 63.6%; Score 1627.5; DB 4; Length 494;
Best Local Similarity 63.1%; Pred. No. 2.2e-172;
Matches 311; Conservative . 73; Mismatches 96; Indels 13; Gaps 6;
QY 1 MGFAMDO--TPLLSKNAIGDGHGESSPYDGWKAYDQNPFFHPDNPNGVMQGLAENQL 58

Qy 1 MGFKAMDQ--TPLLKMAIGDGHGESSPYFDGWKAYDQNPFFHTDNPNGVMQMGLAENQL 58

Db	1	MGFHQDIERQALLSKIAIDDDHGENSAYFDGKWAYDNNPFPENNPGLVIOGMLAEQOL	60
QY	59	TSDLVEDWILLNNPEASICTPEGINDFRAITANQDXYHGLAEFRNAVAKFMARTGRNIRTFD	118
Db	61	SFGMIVDWIRKHPPEASICTPEGLEKFSIANQDXYHGLQEFKAMASPMGKVRGGRVKFD	120
QY	119	PDRIVMSGGATGAHEVATACLADPGGAFLVPYPYPGDFORDLRWRTGVKLVPMVDCSSNN	178
Db	121	PSRIVMGGATGASETIVIFCLADPGDAFLVSPYYAAFDOLDLKWRTAQIIPVHCNSSNN	180
QY	179	FVLTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVWSPINEKRIHLVCD	238
Db	181	FQTEARALEYAKOAGANKVKAGVIITNPSNPLGTYTDRLTKLVTFVNOHDHLICD	240
QY	239	EIYAAVFSOPGISIAEILEDDETECDORNLVHIVYLSKDMGFGFVRGVIYSYNDAV	298
Db	241	EIYATVFKAPTFTSIAEIVEQME--HCKELIHILYLSKDMGLPGFVRGVIYSYNDAV	298
QY	299	VNCARKMSSGLVSTQYQYLLASNLNDDEFVERFLAESAKRLAQRPRVTTGGLAKVGIKC	358
Db	299	VRARQMSFGLVSSQTHLLAAMLDEDFVDKFLAENSKRLGERHARTTKELDKMGITC	358
QY	359	LOSAGLEVWMDLROLLKKPTEDSETELMKVITHEVKINVSPGYSPHCTEPCGWERVCYAN	418
Db	359	LNSNAGVFWMDLURLLKDOTFKAEMLRWIINEVKLVNSPGSSPHVTEPGWFRVCFAN	418
QY	419	MDMAVQIAQLORINFY--LQNK-----VVSNNKKHCWHSNLR--SLKTRRFD--DIWMS	469
Db	419	MDONTVDVALNRHSFVENIDKKEDNTVAMPSTRIHRDNKRLSLYSFSGRRYDKGNVLNS	478
QY	470	PHSPLOSPMVK 482	
Db	479	PHTMSPHPLVRA 491	

RESULT 15

US-08-378-313-29

; Sequence 29, Application US/08378313

; Patent No. 6207881

; GENERAL INFORMATION:

; APPLICANT: THEOLOGIS, ATHANASIOS

; APPLICANT: SATO, TAKAHIDO

; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH

; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/378,313

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/862,493

; FILING DATE: 02-APR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 29190-20002.20

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 856-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

RESULT 15

US-08-378-313-29
; Sequence 29, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/378.313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 7061141

; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-378-313-29

Query Match 63.6%; Score 1627.5; DB 4; Length 494;
Best Local Similarity 63.1%; Pred. No. 2.e-172;
Matches 311; Conservative 73; Mismatches 96; Indels 13; Gaps 6;

QY	1	MGFKAWDQ--TPLLSKAIGDGHGSSPYFDGKAYDQNPFPHTDNPNGVMQGLAENQL	58
Db	1	MGFHQIDERNQALLSKIAIDDHGSENSAYFDGKAYDNNPFPENPLGVIQMGLAENQL	60
QY	59	TSDLVEDRLNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFWATRGHRIYFD	118
Db	61	SEGMIVDWIRKHPASICTPEGLEKFKSIANFQDYHGLQEFKAMASFMGKYRGGVRKFD	120
QY	119	PDRIVMSGGATCAHEVTAFCCLADPGAEFLVPIYPYPGFDRDLRWRTGVKLVPMGDSNN	178
Db	121	PSRIVGGGATGASTVIFCLADPGDAFLVSPYYAATFDRDLKWRTRAQIIPVHCNSSNN	180
QY	179	FVLTKEALEDAYEKAREDNIRVKLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCD	238
Db	181	FQVTEAALEIAYKKAQEAEMKVKGIITNPSNPLGTITVDRDTLKTLTFTVQHDHILCD	240
QY	239	EIYAATVFSQPGFISIAELLEDETIEDCDNLVHIVYSLSKDMGPPGFRVGIYISYNDAY	298
Db	241	EIYSATVFKAPTFTTIAEIVEQME--HCKKELIHLYSLSKDMGLPGFRVGIYISYNDV	298
QY	299	VNCAKMSFGLVSTQTVLLASMLNDDDEFVERFLAESAKRLAQRFRVFTGGSLAKVGIC	358
Db	299	VRRARQMSFGLVSSQTHLLAAMLSDEDFVDKFLAENSKRLGERHARETKELDKWGIC	358
QY	359	LOSAGLFVWMDLROLLKPTFDS TELWKYIIHEVKINVSFGYFCHTEPGWFRVCYAN	418
Db	359	LNSNAGVFVWMDLRLKLDQTFKAEMLRWIINEVKLNVSFGSSFHVTEPGWFRVCYAN	418
QY	419	MDMAVQIALORIRNV--LQNK-----VVVSNKKHCWHSNRL--SLKTRFD--DITMS	469
Db	419	MDNTVDVALNRHISFVENIDKDKDNTVAMPSTKTRHRONKRLSLFSFGRRYDKGNVLNS	478
QY	470	PHSLPQSPMWKA	482
Db	479	PHTMSPHSPLVRA	491

Search completed: August 21, 2002, 02:08:53
Job time: 4743 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2002, 02:01:05 ; Search time 42.72 seconds
(without alignments)
1088.653 Million cell updates/sec

Title: US-09-763-957-2
Perfect score: 2559
Sequence: 1 MGFRAMDQTPLLSKMAIGD.....DITMSPHSLPQSPWVKATN 484

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR71:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2559	100.0	484	2	S26214 1-aminocyclopropan
2	2354	92.0	484	2	S25002 1-aminocyclopropan
3	2115.5	82.7	487	2	T026253 1-aminocyclopropan
4	1791.5	70.0	483	2	T02249 1-aminocyclopropan
5	1781.5	69.6	483	1	T07601 1-aminocyclopropan
6	1750.5	68.4	485	1	T07596 1-aminocyclopropan
7	1747.5	68.3	477	1	T04315 1-aminocyclopropan
8	1739.5	68.0	491	2	T03978 1-aminocyclopropan
9	1721	67.3	490	2	S31450 1-aminocyclopropan
10	1719.5	67.2	487	2	T50552 1-aminocyclopropan
11	1716	67.1	495	2	T13019 1-aminocyclopropan
12	1713	66.9	485	1	S19677 1-aminocyclopropan
13	1709.5	66.8	477	2	T50551 1-aminocyclopropan
14	1701.5	66.5	488	2	T09734 1-aminocyclopropan
15	1667	65.1	491	2	S48827 1-aminocyclopropan
16	1640.5	64.1	493	2	JQ0926 1-aminocyclopropan
17	1640.5	64.1	493	2	T09658 1-aminocyclopropan
18	1636.5	64.0	493	1	A41141 1-aminocyclopropan
19	1635.5	63.9	488	2	T47943 1-aminocyclopropan
20	1627.5	63.6	494	1	B41141 1-aminocyclopropan
21	1626.5	63.6	455	2	S56695 1-aminocyclopropan
22	1620	63.3	518	2	S31442 1-aminocyclopropan
23	1588.5	62.1	486	2	S71583 1-aminocyclopropan
24	1587	62.0	516	2	S19252 1-aminocyclopropan
25	1583	61.9	476	1	S19679 1-aminocyclopropan
26	1578	61.7	496	2	A47199 1-aminocyclopropan
27	1521	59.4	370	2	T10513 1-aminocyclopropan
28	1483.5	58.0	421	2	T08119 1-aminocyclopropan
29	1455	56.9	363	2	S52283 1-aminocyclopropan

30	1435	56.1	366	2	T07827	1-aminocyclopropan
31	1407	55.0	364	2	T17017	1-aminocyclopropan
32	1390.5	54.3	373	2	S52635	1-aminocyclopropan
33	1354.5	52.9	467	2	T10854	1-aminocyclopropan
34	1343.5	52.5	469	2	T06024	1-aminocyclopropan
35	1341	52.4	465	2	S54012	1-aminocyclopropan
36	1341	52.4	473	2	T16999	1-aminocyclopropan
37	1339.5	52.3	475	2	J02214	1-aminocyclopropan
38	1335	52.2	455	2	S56176	1-aminocyclopropan
39	1329.5	52.0	472	1	T10889	1-aminocyclopropan
40	1316.5	51.4	446	2	T17018	1-aminocyclopropan
41	1314	51.3	441	2	S47049	1-aminocyclopropan
42	1309	51.2	447	2	T06004	1-aminocyclopropan
43	1309	51.2	480	2	T06252	1-aminocyclopropan
44	1299	50.8	469	1	A57540	1-aminocyclopropan
45	1295.5	50.6	470	2	S71174	1-aminocyclopropan

ALIGNMENTS

RESULT 1
S26214
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (clone PAIM-1) - mung bean
N;Alternate names: ACC synthase
C;Species: Vigna radiata (mung bean)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-Dec-1999
C;Accession: S26214; S26213; S20919
R;Botella, J.R.; Arteca, J.M.; Schlagnhauser, C.D.; Arteca, R.N.; Phillips, A.T.
Plant Mol. Biol. 20, 425-436, 1992
A;Title: Identification and characterization of a full-length cDNA encoding for an au
of its mRNA in response to indole-3-acetic acid.
A;Reference number: S26213; MUID:93043033
A;Accession: S26214
A;Molecule type: mRNA
A;Residues: 1-484 <BOT>
A;Cross-references: EMBL:Z11613; NID:g22069; PIDN:CAA77688.1; PID:g22070
A;Experimental source: clone PAIM-1
A;Accession: S26213
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 50-415, 'F', 417 <BOF>
A;Cross-references: EMBL:Z11562; NID:g22067; PIDN:CAA77655.1; PID:g22068
A;Experimental source: clone PHIM-1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1992
R;Botella, J.R.; Schlagnhauser, C.D.; Arteca, R.N.; Phillips, A.T.
Plant Mol. Biol. 18, 793-797, 1992
A;Title: Identification and characterization of three putative genes for 1-aminocyclo
A;Reference number: S20919; MUID:92216056
A;Accession: S20919
A;Molecule type: DNA
A;Residues: 27-94 <BOF>
A;Cross-references: GB:M80554; PIDN:AAA53297.1; PID:g170632
A;Experimental source: Rwlilcz cv. Berken, etiolated hypocotyls; clone pMAC-1
C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal pho
F;279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match	100.0%	Score	2559;	DB	2;	Length	484;
Best Local Similarity	100.0%	Pred. No.	4.8e-196;				
Matches	484;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MGFRAMDQTPLLSKMAIGDGHGESSPYFDGKAYDQNFPHPTDNPNGVMQGLAENQLTS	60				
Db	1	MGFRAMDQTPLLSKMAIGDGHGESSPYFDGKAYDQNFPHPTDNPNGVMQGLAENQLTS	60				
QY	61	DLVEDWTLLNPEASICTPEGINFRAITAFQDHYHGLAEFRNAKFMARTGRNRTITDPD	120				
Db	61	DLVEDWTLLNPEASICTPEGINFRAITAFQDHYHGLAEFRNAKFMARTGRNRTITDPD	120				
QY	121	RIVMSGGATGAHEWTFACLDPGFAFLVPIPYPGFDRLRWRTGVKLVPMCDSSNFEV	180				

Db	121	RIVMSGGATGAHEVTAFCCLADPGEAFLVPIPYYPGDFDRDLRWRTGVKLVPMCDSSNNFV	180
Qy	181	LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTLLRTVVSFINEKRHLVCDDEI	240
Db	181	LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTLLRTVVSFINEKRHLVCDDEI	240
Qy	241	YAATVFSQPGFISIAIELEDIEDCDRLNHLVHIVYSLSKDMGFGPFRVGIISYNDVVN	300
Db	241	YAATVFSQPGFISIAIELEDIEDCDRLNHLVHIVYSLSKDMGFGPFRVGIISYNDVVN	300
Qy	301	CARKMSSFGVLSTQTYQLLASMLNDEFERFLAESAARLAQRFRVFTGGLAKVGKICLQ	360
Db	301	CARKMSSFGVLSTQTYQLLASMLNDEFERFLAESAARLAQRFRVFTGGLAKVGKICLQ	360
Qy	361	SNAGLFVWMDLRQLLKKPTFDETELKWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD	420
Db	361	SNAGLFVWMDLRQLLKKPTFDETELKWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD	420
Qy	421	DMAVOIALQIRIRNFVLQNKVVVSNKKHCWHSNLRSLKTRRFDITMSPHSPLPQSPMV	480
Db	421	DMAVOIALQIRIRNFVLQNKVVVSNKKHCWHSNLRSLKTRRFDITMSPHSPLPQSPMV	480
Qy	481	KATN 484	
Db	481	KATN 484	
RESULT	2		
S25002			
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - soybean			
C:Species: Glycine max (soybean)			
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000			
C:Accession: S25002			
R:Li, D.; Li, N.; Mattoo, A. K.			
submitted to the EMBL data library, June 1992			
A:Description: Nucleotide sequence of soybean ACC synthase.			
A:Reference number: S25002			
A:Accession: S25002			
A:Molecule type: mRNA			
A:Residues: 1-484 <LIU>			
A:Cross-references: EMBL:X67100; NID:gl8557; PIDN:CAA47474.1; PID:g18558			
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase			
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosphate			
F:279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted			
Query Match 92.0%; Score 2354; DB 2; Length 484;			
Best Local Similarity 90.9%; Pred. No. 1.1e-179;			
Matches 439; Conservative 21; Mismatches 23; Indels 0; Gaps 0;			
Qy	1	MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTS	60
Db	1	MGKAMDQTPQLLSKMWIGDGHGESSPYFDGWKAYDONPFPKPNPNGVQIOMGLAENQLTS	60
Qy	61	DLVEDWILNPNPASICTPGINDFRAIANFQDYHGLAEFRNAVAKFMATRGNNRTTFDD	120
Db	61	DLVEDWILNPNPASICTPGINDFRAIANFQDYHGLPERNAVAKFMATRGNNRTTFDD	120
Qy	121	RIVMSGGATGAHEVTAFCCLADPGEAFLVPIPYYPGDFDRDLRWRTGVKLVPMCDSSNNFV	180
Db	121	RIVMSGGATGAHEVTTFCCLADPGEAFLVPIPYYPGDFDRDLRWRTGVKLVPMCDSSNNFV	180
Qy	181	LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTLLRTVVSFINEKRHLVCDDEI	240
Db	181	LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTLLRTVVSFINEKRHLVCDDEI	240
Qy	241	YAATVFSQPGFISIAIELEDIEDCDRLNHLVHIVYSLSKDMGFGPFRVGIISYNDVVN	300
Db	241	YAATVFSQPGFISIAIELEDIEDCDRLNHLVHIVYSLSKDMGFGPFRVGIISYNDVVN	300
Qy	301	CARKMSSFGVLSTQTYQLLASMLNDEFERFLAESAARLAQRFRVFTGGLAKVGKICLQ	360
Db	301	CARKMSSFGVLSTQTYQLLASMLNDEFERFLAESAARLAQRFRVFTGGLAKVGKICLQ	360
Qy	421	DMAVOIALQIRIRNFVLQNKVVVSNKKHCWHSNLRSLKTRRFDITMSPHSPLPQSPMV	480
Db	421	DMAVOIALQIRIRNFVLQNKVVVSNKKHCWHSNLRSLKTRRFDITMSPHSPLPQSPMV	480

Qy	361	SNAGLFVWMDLRQLLKKPTFDETELKWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD	420
Db	361	SNAGLFVWMDLRQLLKKPTLDEMEELRWIIDEVKINVSFGSFSFHCTEPGWFRVCYANMD	420
Qy	421	DMAVOIALQIRIRNFVLQNKVVVSNKKHCWHSNLRSLKTRRFDITMSPHSPLPQSPMV	480
Db	421	DMAVOIALQIRIRNFVLQNKVVVSNKKHCWHSNLRSLKTRRFDITMSPHSPLPQSPMV	480
Qy	481	KAT 483	
Db	481	KAT 483	
RESULT	3		
T06253			
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 2 - garden pea			
C:Species: Pisum sativum (garden pea)			
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000			
C:Accession: T06253			
R:Peck, S.C.; Kende, H.			
Plant Mol. Biol. 38, 977-982, 1998			
A:Title: Differential regulation of genes encoding 1-aminocyclopropane-1-carboxylate			
A:Reference number: Z15569; MUID:99084749			
A:Accession: T06253			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-487 <PEC>			
A:Cross-references: EMBL:AF016459; NID:g2360988; PIDN:AAD04199.1; PID:g2360989			
C:Genetics:			
A:Gene: ACS2			
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase			
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosphate			
F:279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted			
Query Match 82.7%; Score 2115.5; DB 2; Length 487;			
Best Local Similarity 81.1%; Pred. No. 1.1e-160;			
Matches 394; Conservative 47; Mismatches 42; Indels 3; Gaps 2;			
Qy	1	MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTS	60
Db	1	MGVWMLDQPLLKSKIAMGDGHGESSPYFDGWKAYDKDPHPKSNPHGVQIOMGLAENQLTA	60
Qy	61	DLVEDWILNPNPASICTPGINDFRAIANFQDYHGLAEFRNAVAKFMATRGNNRTTFDD	120
Db	61	DMVQNMKSNPASICTLGTVHNFQMANFQDYHGLPEFRNAVAKFMSTRGNRTTFDPE	120
Qy	121	RIVMSGGATGAHEVTAFCCLADPGEAFLVPIPYYPGDFDRDLRWRTGVKLVPMCDSSNNFV	180
Db	121	RIVMSGGATGAHEATAFCLADRGAEALLVPTPYPGDFDRDLRWRTGVKLVPMCDSSNNFV	180
Qy	181	LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTLLRTVVSFINEKRHLVCDDEI	240
Db	181	LTQKALEEAYEKAREDNIRFKGLLITNPSNPLGTVMDRNTLRTVITFINEKRHLISDEI	240
Qy	241	YAATVFSQPGFISIAIELEDIEDCDRLNHLVHIVYSLSKDMGFGPFRVGIISYNDVVN	300
Db	241	YAATVFSHPFSFISIAIEIIEHDIEDCDRLNHLVHIVYSLSKDMGFGPFRVGIISYNDVVN	300
Qy	301	CARKMSSFGVLSTQTYQLLASMLNDEFERFLAESAARLAQRFRVFTGGLAKVGKICLQ	360
Db	301	CPYKMSFGVLSTQTYQLIAKMLSDDDPVEKFLSAKRLAQRVFTGGLKVGKICLQ	360
Qy	361	SNAGLFVWMDLRQLLKKPTFDETELKWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD	420
Db	361	SNGLFVWMDLRGLLKNATFESEIELRWVIIHEVKINVSFGYSFHCSEPGWFRVCYANMD	420
Qy	421	DMAVOIALQIRIRNFVLQ - NKEVVS - - NKKHCWHSNLRSLKTRRFDITMSPHSPLPQS	477
Db	421	DRDVOIALQIRIRSFVTQNNKEAMGSKSKPKYWHWSNLRSLKPRRFDITMSPHSPIPQS	480
Qy	478	PMVKAT 483	

Db 481 PLVRAT 486

1:|||||

RESULT 4
T02249

1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - common tobacco
N:Alternate names: ACC synthase
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 20-Jun-2000
C:Accession: T02249
R:Weterings, K.; Perzotti, M.; Cornelissen, M.; Mariani, C.
Submitted to the EMBL Data Library, June 1996
A:Description: Pollination induced ACC-synthase and ACC-oxidase expression.
A:Reference number: Z14638
A:Accession: T02249
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-483 <WET>
A:Cross-references: EMBL:X98492; PIDN:CAA67118.1
C:Genetics:
A:Gene: ACCS2
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph
F;278/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Q7	71	FEASLCI	FEINDT	NALANT	VDI	HGAREF	KNAAVE	MAKIR	GNKRLT	DPDKI	VMSGGATG	133
		:		:	:							
Dh	73	PRASITVE	GAENFODIA	TODNVCI	DEEPO	AVAREMP	VPCDNYEN	DNBNB	TVMSCC	AMC		133

131 AHEVTAFLADGCEAFLVPIPPYPGDRDLRWRTGVKLVPMCDSSNNFVLTKEALEDAY 190

QY 191 EKAREDNIRVKGILLITNSPNPLGTINDRKTLTVVSFINKRIHLVCDIEIYAATVFSQPG 250

[illegible]

QY 311 VSTQTYLLASMLNDDFEVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370

QY 371 L RQLKKPTFDSTELWKVIIHEVKINVS PGSPHCTEPGWFRCVYANMDDMAVQIALQR 430

Qy 431 IRNFVLONKEV--VWSNKHCWCHSNJLSLSKTRFEDDITNMPHSPLPQSPWVK 481

DD 431 IRNEVLQTKGLNNIAAIRKQCSRSKLQISLSFRRLDDFNPAHSPN-NSPLVR 482

T07596
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 1A - tomato

C.Species: *Mycooperison escurientum* (tomato)
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C.Accession: M07596

A:Description: LE-ACS1A and LE-ACS1B, duplicated genes encoding 1-aminocyclopropane carboxylate synthase
A:Reference number: Z16039
A:Accession: T07596
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A: Status: translated from GB/EMBL/DDBJ
A: Molecule type: mRNA

A:Residues: 1-485 <OON>
A:Cross-references: EMBL:U72389; NID:g1621640; PIDN:AAB17278.1; PID:g1621641
A:Experimental source: cultivar Rutgers; clone PLEACS1A3
C:Genetics:
A:Gene: ACS1A
C:Function:
A:Description: catalyzes the conversion of S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate
A:Pathway: ethylene biosynthesis
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph
F:279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

	Query Match	Best Local Similarity	Score	DB 1;	Length	DB 2;
	Matches	Conservative	326;	Mismatches	66;	Indels
						Gaps
Qy	11	LLSKWATGDGHCESPFDGKWKAYDONPFHPTDNPNGVQMGLAENQLTSLDVEDWILNN	70			
Db	13	LLSKIATNDGHCENSPFDGKWKAYANPNFHLTDNPTGVIQMGLAENQLCFDLIQEWYVNN	72			
Qy	71	PEASICTPEGINDIRATNFQDHYHGLAEFRNAVAKEMARTGRNITTFDPRDRTVMSGGATG	130			
Db	73	PKASICTVEGAENFQDIAFDYHGLPEFRQAVAREMEKVRGDRVTFDPNRIYVMSGGATG	132			
Qy	131	AHEVTAFLADPGAEFLVPIPYEGFDRDLRWRTGVLKVPVCMDSNNFVLTKALEDAY	190			
Db	133	AHEMLAFCLADPGDAFLVPTPYPGFDRDLRWRTGVLKFPVVCESCNDKFKVTTKALEAY	192			
Qy	191	EKAREDNIRKGLLITNPSNPLGTIMDRKTLRTVVVSFINKRIHLVCDIYAATVFSQFG	250			
Db	193	EKAQSNIKIKGLLITNPSNPLGTILDKDTRLDIVTFINSKNIHLVCDIYAATVFDQPR	252			
Qy	251	FISIAEILEDTECDRLNLIHIVISLSKDMGFGFGRVGIIVSYNDVAVNCARKMSSFGL	310			
Db	253	FISVSEIVEDM--TECNKDLIHIIVISLSKDLGFFGFRVGIIVSYNDVAVNCARKMSSFGL	310			
Qy	311	VSTQTVLLASMLNDEDFEFLAESAKRLAQRFRVFTGGKLVKIKQLSQSNAGLFFVMD	370			
Db	311	VSAQTQHLASMLSDEVFIDFKFAESSRIGERQGMFTKGLAEVSGISTLKSNAGLFFVMD	370			
Qy	371	LROLLKPTFDSETELKWKVIHEKINVSFGYSHCTEPGHWFRVCYANMDMVAOIALQR	430			
Db	371	LRLLEKATFDSELELWRITIIINEVKNLVSQCSFEPGHWFRVCYANMDDETMTIALKR	430			
Qy	431	IRNFVLQNKVE--VVSNNKHCQHSNLRSLSLKTRFDDITMSP-HSPLPQSPMVK	481			
Db	431	ISYFVLQPKGLNNIAIKQCSRKLQISLSFRRLDHEFMNSPAHSPM-NSPLVR	484			

RESULT 7
T04315
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - tomato
N:Alternate names: ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase
C:Species: Lycopersicon esculentum (tomato)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Jun-2000
C:Accession: T04315
R:Nakajima, N.; Bae, G.; Saji, H.; Aono, M.; Kubo, A.; Kondo, N.
submitted to the EMBL Data Library, April 1998
A:Description: Rapid accumulations of transcripts of ethylene biosynthesis enzymes in
A:Reference number: Z15278
A:Accession: T04315
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-477 <NAK>
A:Cross-references: EMBL:AB013346; PIDN:BA25916.1
A:Experimental source: tissue-type green leaves
C:Function:
A:Description: catalyzes the conversion of S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate
A:Pathway: ethylene biosynthesis
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph
F:269/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match	68.3%;	Score 1747.5;	DB 1;	Length 477;
Best Local Similarity	69.5%;	Pred. No. 2.4e-131;		
Matches 332;	Conservative 66;	Mismatches 73;	Indels 7;	Gaps
Qy 11	LLSKMAIGDHGESSPYFDGHWKAYDQNPFTDNPNGVMQGLAENOLTSDLVEDTILNN 70			
Db 3	LISKIATNDHGCHNSAFYDGHKAYENDPFHTQNPNGVIOQLAENOLCFDLQIQLVNN 62			
Qy 71	PEASICTPEGINDPRAIANFQDYHGLAEFRNAKAFMARTGRNITDPDRIVMSGGATG 130			
Db 63	PKASICTYEGVQDFQDAIFODYHGLPEFRKAVAREMEKVRGDRVRDPERIVMSGGATG 122			
Qy 131	AHEVTAECIADPGGAFLVPTPYPGCFORDLRWRTGVKLVPVMDSSNNFVLTKEALEDAY 190			
Db 123	AHESLAFCLADPGGAFLVPTPYPGCFORDLRWRTGVQLFPVVCSSNNFVLTKEALEEAY 182			
Qy 191	EKAREDNIRVKGLLITNPSNPLGTHIMDKTLRTVVSFINCKRIHLVCDEIYAATVFSQPQ 250			
Db 183	SKAQESNIKYVKGLLINPNSNPLGTILDKETLKDILREFINDKNIHLVCDEIYAATFSQPS 242			
Qy 251	FISTAEILEDTETEDCNLNVHVIYSLSKMDGPPGFRVGYIYSYNDADVNCARKMSSFGL 310			
Db 243	FISISEVKSEY--VGCNDLNVHVIYSLSKDLGPFEGFRVGYIYSYNDADVNAIARKMSSFGL 300			
Qy 311	VSTQTYLLASMLMDDFEVERFLAESAKRLAQRPRVFTGLGKVGIKQLQSNAGLFWMD 370			
Db 301	VSTQTRLIASMLLDTIFVEDFIKSSMRLLQRYGLTGLGQGVITTLASNAGLFIWMD 360			
Qy 371	LROLKKPTTFSTELKWKVIIHEWKVINSVGYSPHCTEPGWFRVCYANMDMVAQIALQR 430			
Db 361	LRRFLEINSTFDELKLHHIIIDTKVLNVSPGSCSPHCSEPGWFRVCFANMDATMKIALRR 420			
Qy 431	IRNRFV-LQ-NKEVNVVSKK-HC-WHSNLRLSLTKRRRDDITMSPHSPLQSPMVKATN 484			
Db 421	IRHFVYLOPNKSGVEATKKQYCRTRFSKLEISLSLFRLLDFMNSPHSPM--SSPVMQARN 477			
RESULT	8			
T03978				
C:Species	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - common tobacco			
C:Date	23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Jan-2000			
C:Accession	T03978			
R:Bailey, B.A.; Avnii, A.; Li, N.; Matoo, A.K.; Anderson, J.D.				
Plant Physiol.	100, 1615-1616, 1993			
A:Title	Nucleotide sequence of the Nicotiana tabacum cv Xanthi gene encoding			
A:Reference number	215173			

[illegible]

Db 121 RVVMAGGATGANETIIIFCLADTGAFLVPSYPYAFNRDLRWRTGVQLIIPICDSSNNFQ 180
QY 181 LTVKALEADAYEKAREDIRVVKGLLTNPNSNPLGTIMDRKTLRTVVSFINERKHLVCEDEI 240
Db 181 ITTKAVREAYENAKSNIKVGLILTNPSNPLGTITLDRDTLKNLLTFNQHNHLVCEDEI 240
QY 241 YAATVFSQPGFISATLEDETIEDCRNLVHIVISLSKDMGPGFVRVGIISYNDVAVN 300
Db 241 YAATVNTPOFVSIAETLDDTS-HCNKDLVHIVISLSKDMGLPGFVRVGIISYNDVAVN 299
QY 301 CARMSFGLVSTQTOYLLASMLNDDFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQ 360
Db 300 CARMSFGLVSTQTOYLLAEMLSDERFVSFNTESKRLAKRKHHTNGLAEVGIKCLR 359
QY 361 SNAGLFVMDLRQLLKKPTDSETELKWKIHEVKINVSFGYSPHCTEPGWFRVCYANMD 420
Db 360 SNAGLFVMDLRQLLKKPTDSETELKWKIHEVKINVSFGYSPHCTEPGWFRVCYANMD 419
QY 421 DMVAOIALORIRNFVQLNKE- - - - -VVVSNKKHCW-HSNLRLSLKTRRFD-ITMSP-HS 472
Db 420 DETVDALARIRFVGKKSDESTPILMEKKQMKNNLRLSFRKMYDESVLSPSS 479
QY 473 PLPQSPMVK 482
Db 480 PIPHSPLVRA 489

RESULT 9

S31450
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C:Accession: S31450
R:Michael, M.Z.; Baudinette, S.C.; Savin, K.W.; Cobbett, C.S.; Cornish, E.C.
submitted to the EMBL Data Library, December 1992
A:Description: Isolation of petal senescence-associated cDNA clones encoding 1-aminocyclopropane-1-carboxylate synthase
A:Reference number: S31450
A:Accession: S31450
A:Molecule type: mRNA
A:Residues: 1-490 <MIC>
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosphate
F:277/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 67.3%; Score 1721; DB 2; Length 490;
Best Local Similarity 65.4%; Pred. No. 3.2e-129;
Matches 320; Conservative 73; Mismatches 88; Indels 8; Gaps 4;
QY 1 MGPKAMDQTPLLSKMAIGDGHGSSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTS 60
Db 1 MGPESEKNNSVLSKLTATNEHGENSPYFDGWKAYDNDPFPKLPNGVIOQGLAENQLCF 60
QY 61 DLVEDTLNNEASICTPEGINDFRATNFQDHYGLAEFRNAVAKFMARTGNRITDPD 120
Db 61 DLLEDWIKRNPASICTTEGIKSGFRATNFQDHYGLAEFRRAIAKFMKTRGRVSPDP 120
QY 121 RYVMSGGATGAHEVTAFCLADPGAEFLVPIPYPGFDRDLRWRTGVKLVPMVDCSSNNFV 180
Db 121 RVVMAGGATGANETIIIFCLADAGAFVPSYPYAFNRDLRWRTGVQLIIPICSSNSFK 180
QY 181 LTVKALEADAYEKAREDIRVVKGLLTNPNSNPLGTIMDRKTLRTVVSFINERKHLVCEDEI 240
Db 181 ITTKAMKEAYENAKIRVVKGLILTNPSNPLGTITLDRDTLKSLLNFTNERNHLVCEDEI 240
QY 241 YAATVFSQPGFISATLEDETIEDCRNLVHIVISLSKDMGPGFVRVGIISYNDVAVN 300
Db 241 YAATVNTPOFVSIAETLDDTS-HCNKDLVHIVISLSKDMGLPGFVRVGIISYNDVAVN 299
QY 301 CARMSFGLVSTQTOYLLASMLNDDFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQ 360
Db 300 CARMSFGLVSTQTOYLLAEMLSDERFVSFNTESKRLAKRKHHTNGLAEVGIKCLR 359

Db 300 CARMSFGLVSTQTOYLLAKMLSDSEEFVANFLCESSMRLGKRKHHTNGLAEVGIKCLR 359
QY 361 SNAGLFVMDLRQLLKKPTDSETELKWKIHEVKINVSFGYSPHCTEPGWFRVCYANMD 420
Db 360 SNAGLFVMDLRQLLKKPTDSETELKWKIHEVKINVSFGYSPHCTEPGWFRVCYANMD 419
QY 421 DMVAOIALORIRNF- - - - -VLQNKEVV- - - - -VSNKKHCWHSNLRSLKTRRFDITMSP-HSP 473
Db 420 DETVEVALARIRFVGKVGKENGEBTPVKNKQKWSNLRKYSFRKMYDESVLSPSS 479
QY 474 LPQSPMVK 482
Db 480 IPHSPLVRA 488

RESULT 10

T50552
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) acsl [similarity] - white lupine
C:Species: Lupinus albus (white lupine)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000
C:Accession: T50552
R:Bekman, E.P.; Saibo, N.J.M.; Di Cataldo, A.; Regalado, A.; Pinto Ricardo, C.; Rodri
submitted to the EMBL Data Library, January 1999
A:Description: Four genes encoding 1-aminocyclopropane-1-carboxylate synthase in Lupi
A:Reference number: 225126
A:Accession: T50552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-487 <BEK>
A:Cross-references: EMBL:AF119411; PIDN:AAF22109.1
C:Genetics:
A:Gene: ACS1
C:Function:
A:Pathway: ethylene biosynthesis
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C:Keywords: carbon-sulfur lyase; phosphoprotein; pyridoxal phosphate
F:277/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 67.2%; Score 1719.5; DB 2; Length 487;
Best Local Similarity 66.3%; Pred. No. 4.2e-129;
Matches 320; Conservative 74; Mismatches 74; Indels 15; Gaps 5;
QY 11 LLSKMATGDCGHGSSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTSLDVEDTLNN 70
Db 10 LLSKIATNDKHGENSPYFDGWKAYDNNPFPKLPNGVIOQGLAENQLCFDLEIWKNN 69
QY 71 PEASICTPEGINDFRATNFQDHYGLAEFRNAVAKFMARTGNRITDPDPRIVMSGGATG 130
Db 70 PKASICTLEGVHKFRDIAFODYHGLPEFRNALANFMSKVRGNGVRFPDPRIVMSGGATG 129
QY 131 AHEVTAFCLADPGAEFLVPIPYPGFDRDLRWRTGVKLVPMVDCSSNNFVLTKEALEDAY 190
Db 130 ANEVIMECLADPGAEFLVPIPYPAFLDLRDLRWRTGVKLVPMVDCSSNNFVLTKEALEKAY 189
QY 191 EKAREDIRVVKGLLTNPNSNPLGTIMDRKTLRTVVSFINERKHLVCEDEIYAATVFSQPG 250
Db 190 NKAKEDINVKGLITNPNSNPLGTITLDRDLKSLITFINENNNHLVCEDEIYAATVFSQPS 249
QY 251 FISTAEILEDETIEDCRNLVHIVISLSKDMGPGFVRVGIISYNDVAVNCAKMSFGL 310
Db 250 YVSVSELIQ-EMQPCCKDLHIIISLSKDMGPGFVRVGIISYNDVAVNCAKMSFGL 308
QY 311 VSTQTOYLLASMLNDDFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQSNAGLFVMD 370
Db 309 VSSQTOYLLASMLSDSDSFVDKFLAESKRLAKRKHHTNGLAEVGIKCLR 368
QY 371 LRQLLKKPTDSETELKWKIHEVKINVSFGYSPHCTEPGWFRVCYANMDMAVOIALQR 430
Db 369 LKSLLEKQTEAEAMMLWHMIINVKLVNVSFGYSPHCSEPCWFRVCYANMDDETVEALTR 428
QY 431 IRNFV- - - - -LQNKEVVSNKKHCWHSNLRSLKTRRFDIT- - - - -MSPSPLPQSPMV 480

Db 429 INTFGKTKKDEMVKQK-----WQRNLQSFSSIRRFVHETIMSPHMMSPHSPIQSPLV 484

Qy 481 KAT 483

Db 485 KAT 487

RESULT 11

T13019

1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) ACS-6 - Arabidopsis thaliana

N:Alternate names: ACC synthase; protein F8L21.70

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 04-Feb-2000

C:Accession: T13019

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew

submitted to the Protein Sequence Database, July 1999

A:Reference number: 217587

A:Accession: T13019

A:Molecule type: DNA

A:Residues: 1-495 <BEV>

A:CROSS-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.70

A:Experimental source: cultivar Columbia; BAC clone F8L21

C:Genetics:

A:Gene: ACS-6; ATSP:F8L21.70

A:Map position: 4

A:Introns: 60/3; 104/3; 158/2

C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase

C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph

F:280/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 67.1%; Score 1716; DB 2; Length 495;

Best Local Similarity 66.8%; Pred. No. 8.2e-129;

Matches 322; Conservative 59; Mismatches 89; Indels 12; Gaps 3;

Qy 11 LLSKMAIGDGHGESSPYDQGWKAYQDNFPHPTDNPNGVMQGLAENQLTSLDVEDWILNN 70

Db 14 LLSKIASGDGHGENSESYDQGWKAYENPFHPTDRPDGVQIOMGLAENLCCGLDMRRKWLKH 73

Qy 71 PEASICTPEGINDFRAINFQDYGHLAEFRNAVAFMARTNRTTFDPDRIVMSGGATG 130

Db 74 PEASICTSEGVNQFSDIAIFQDYGHLPEFRQAVAFMEKTRNKKVKFDPDRIVMSGGATG 133

Qy 131 AHEVTAFLADPGEAFLPIPYPGFDRDLRWRTGKLVPMCDSSNNFVLTKEALDAY 190

Db 134 AHETVAFCLANPDGFLVPTPYPGFDRDLRWRTGCVNLVPTTCHSSNGFKITVEALEAAY 193

Qy 191 EKAREDNIRVGLLTNPNSPLGTTMDRKTLETVVYFNEKRIHLVCDIEIYAATVFSQPG 250

Db 194 ENARKSNIPVKGLLTNPNSPLGTTMDRCLKSLNFTNDKGIHLIADEIYAATVFGQSE 253

Qy 251 FLISAEILEDETDIECDRLNLHVIVYSLSKDMGFGPFRVGIYISNDVYVNCARKMSSFGL 310

Db 254 FLISAEVIEEIED--CNRDLIHIVYSLSKDMGLPGLRGVIVSYNDRVVQIARKMSSFGL 311

Qy 311 VSTQYQYLLASMLNDEPFVERFLAESAQLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370

Db 312 VSSQTHLIATKLSDEEFDVDFIRESKLRLAARHAEITTLGDLGIGLWKLAKAGLFLWMD 371

Qy 371 LRQLLKKPTFDSSETELWKVIIHEVINYPGVSFFHCTEPGFRCVYANWDMVAQIALQR 430

Db 372 LRNLKLTATFDSSETELWRVIVHQVKNLYNSPGGSPFHCEPFGFRVCFANFDMHDKMTETALAR 431

Qy 431 IRNFVLOQKE-----VVYSNKKHCWHSNLRSLK--TRRFDDITSPSPHPLQSPSPV 480

Db 432 INVFTSOLEETEKPMAYTTHMAKKKKCKQSNLRLSFSFSDTRFRDDGTFSPHSFPVPPSPLV 491

Qy 481 KA 482

Db 492 RA 493

RESULT 12

SI9677

1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 2 - tomato

N:Alternate names: ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase

C:Species: Lycopersicon esculentum (tomato)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999

C:Accession: SI9677; SI9678; S24358; B36201; A35516; A41985; B33103

R:Rottmann, W.H.; Peter, G.F.; Oeller, P.W.; Keller, J.A.; Shen, N.F.; Nagy, B.P.; Ta

J. Mol. Biol. 222, 937-961, 1991

A:Title: 1-aminocyclopropane-1-carboxylate synthase in tomato is encoded by a multiple

A:Reference number: SI9677; MUID:92106351

A:Accession: SI9677

A:Molecule type: DNA

A:Residues: 1-485 <ROT>

A:CROSS-references: EMBL:X59139; NID:g19165; PIDN:CAA41855.1; PID:g19166

A:Genetics: ACC

A:Accession: SI9678

A:Molecule type: mRNA

A:Residues: 1-123,'V',125-485 <ROW>

A:CROSS-references: EMBL:X59145; NID:g19167; PIDN:CAA41856.1; PID:g19168

R:Li, N.; Wiesman, Z.; Liu, D.; Mattoo, A.K.

FEBS Lett. 306, 103-107, 1992

A:Title: A functional tomato ACC synthase expressed in Escherichia coli demonstrates

A:Reference number: S24358; MUID:92339529

A:Accession: S24358

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 9-485 <LIN>

A:CROSS-references: EMBL:X62536; NID:g19163; PIDN:CAA44397.1; PID:g19164

A:Experimental source: cv. Pix-Red

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

R:Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.

Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990

A:Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-

A:Reference number: A36201; MUID:91045911

A:Accession: B36201

A:Molecule type: protein

A:Residues: 275-286 <YIP>

R:Van Der Straeten, D.; Van Wiemeersch, L.; Goodman, H.M.; Van Montagu, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 4859-4863, 1990

A:Title: Cloning and sequence of two different cDNAs encoding 1-aminocyclopropane-1-

A:Reference number: A35516; MUID:90280476

A:Accession: A35516

A:Molecule type: mRNA

A:Residues: 1-321,'P',323-398,'L',400-485 <VAN>

A:CROSS-references: GB:M34289; NID:g170363; PIDN:AAA81580.1; PID:g170364

R:Yip, W.K.; Moore, T.; Yang, S.F.

Proc. Natl. Acad. Sci. U.S.A. 89, 2475-2479, 1992

A:Title: Differential accumulation of transcripts for four tomato 1-aminocyclopropane

A:Reference number: A41985; MUID:92196141

A:Accession: A41985

A:Molecule type: mRNA

A:Residues: 208-310 <YI2>

A>Note: sequence extracted from NCBI backbone (NCBIN:88505, NCBIP:88522)

C:Genetics: <ACC>

A:Gene: ACC2

A:Introns: 57/3; 100/3; 154/2

C:Function:

A:Description: catalyzes the conversion of S-adenosylmethionine to 1-aminocyclopropan

A:Pathway: ethylene biosynthesis

C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase

C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal pho

F:278/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 66.9%; Score 1713; DB 1; Length 485;

Best Local Similarity 65.6%; Pred. No. 1.4e-128;

Matches 319; Conservative 72; Mismatches 89; Indels 6; Gaps 4;

Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYDQGWKAYQDNFPHPTDNPNGVMQGLAENQLTS 60

Db 1 MGFEAKTNSILSKLATNEHGENSPYDQGWKAYSDPFPPLKNPNGVQIOMGLAENQLCL 60

QY 191 EKAREDNIRVKGLLITNPSNPLGTTMDRKTLRTVVSFINEARHLVLCDEIYAATVFSQPG 250

Qv 370 DIBOLKKPPTDSETELKWKVIIHEVKIN'VSPGYSFHCTEPGWERYCYANMDDMAVOIALO 4299

Qv 370 DIBOLKKPPTDSETELKWKVIIHEVKIN'VSPGYSFHCTEPGWERYCYANMDDMAVOIALO 4299

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OM protein - protein search, using sw model

Run on: August 21, 2002, 02:08:10 ; Search time 66.98 Seconds

(without alignments)

1250.068 Million cell updates/sec

Title: US-09-763-957-2

Perfect score: 2559

Sequence: 1 MGRAMDQTPLLSKMAICDG.....DITMSPHPLPQSPMVKATN 484

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2559	100.0	484	10	Q43858 phaseolus a
2	2115.5	82.7	487	10	O22464 pisum sativ
3	1945	76.0	487	10	Q9MB64 malus domes
4	1922	75.1	489	10	P93772 pelargonium
5	1913	74.8	487	10	Q9MB65 malus domes
6	1881.5	73.5	481	10	Q9MB76 populus eup
7	1876	73.3	490	10	Q9FEM2 cucumis mel
8	1874	73.2	490	10	Q9MB85 cucumis mel
9	1873.5	73.2	483	10	Q9S711 citrus sine
10	1863.5	72.8	489	10	O82124 cucumis sat
11	1823	71.2	487	10	Q9ZRC8 carica papa
12	1791.5	70.0	483	10	O49904 nicotiana t
13	1785.5	69.8	485	10	Q94116 cucurbita m
14	1781.5	69.6	483	10	Q96580 lycopersico
15	1781	69.6	482	10	O65328 nicotiana g
16	1776	69.4	484	10	O65210 nicotiana g

17	1771.5	69.2	483	10	Q9S853 lycopersico
18	1765.5	69.0	486	10	Q9FXS0 solanum tub
19	1764	68.9	484	10	Q9SC82 nicotiana t
20	1762.5	68.9	486	10	Q9MB75 populus eur
21	1755.5	68.6	485	10	Q9S854 lycopersico
22	1750.5	68.4	485	10	Q96579 lycopersico
23	1747.5	68.3	477	10	P93235 lycopersico
24	1743.5	68.1	477	10	Q94GA2 lycopersico
25	1740.5	68.0	477	10	Q9SAZ4 lycopersico
26	1735.5	67.8	489	10	O49123 rumex palus
27	1732	67.7	486	10	O81636 musa acumin
28	1721	67.3	490	10	O43813 petunia hyb
29	1719.5	67.2	487	10	Q9SEJ9 lupinus alb
30	1719.5	67.2	485	10	Q9SXN9 pyrus pyrif
31	1717.5	67.1	485	10	Q9MWJ6 musa acumin
32	1716	67.0	495	10	Q9SUT3 arabidopsis
33	1714	67.0	486	10	Q9SLY6 musa acumin
34	1712	66.9	486	10	Q9SVT9 musa acumin
35	1711.5	66.9	492	10	O9LRC1 prunus pers
36	1709.5	66.8	477	10	Q9SMH1 citrus sine
37	1701.5	66.5	488	10	O49819 carica papa
38	1701.5	66.5	489	10	O65209 nicotiana g
39	1700	66.4	477	10	P94005 lycopersico
40	1693.5	66.2	482	10	Q43810 pelargonium
41	1674	65.4	486	10	O65841 musa acumin
42	1667	65.1	491	10	Q43747 brassica ol
43	1652	64.6	486	10	O82719 arabidopsis
44	1651.5	64.5	493	10	Q9MB86 cucumis mel
45	1648.5	64.4	459	10	O82679 citrus sine

ALIGNMENTS

RESULT 1

ID	Q43858	PRELIMINARY;	PRT;	484 AA.
AC	Q43858;			
DT	01-NOV-1996 (Tremblrel. 01, Created)			
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	1-AMINOCYCLOPROPANE 1-CARBOXYLATE SYNTHASE (EC 4.4.1.14).			
OS	Phaseolus aureus (Mung bean) (Vigna radiata).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.			
OX	NCBI_TaxID=3916;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=RWILCZ, AND CV. BERKEN; TISSUE=ETIOLATED HYPOCOTYL;			
RX	MEDLINE=93043033; PubMed=1421146;			
RA	Botella J.R., Artega J.M., Schlagnhauser C.D., Artega R.N.,			
RA	Phillips A.T.;			
RT	"Identification and characterization of a full-length cDNA encoding			
RT	for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from			
RT	etiolated mung bean hypocotyl segments and expression of its mRNA in			
RT	response to indole-3-acetic acid.";			
RL	Plant Mol. Biol. 20:425-436(1992).			
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC			
CC	ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT			
CC	AMINOTRANSFERASES.			
CC	EMBL; Z11613; CAA77688.1; -.			
DR	HSSP; P37821; 1B8G.			
DR	InterPro; IPR001176; ACC_synthase.			
DR	InterPro; IPR001511; Aminotran_1.			
DR	Pfam; PF00155; aminotran_1_2; 1.			
DR	PRINTS; PR00753; ACCSYNTHASE.			
DR	PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.			
KW	Lyase; Pyridoxal phosphate.			
SQ	SEQUENCE 484 AA; 54646 MW; E55338B0F7F71478 CRC64;			

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Query Match      100.0%; Score 2559; DB 10; Length 484;
Best Local Similarity 100.0%; Pred. No. 3.9e-195;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNFPHFTDNPNGVQMGGLAENQLTS 60
   |||||
Db 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNFPHFTDNPNGVQMGGLAENQLTS 60
   |||||

Qy 61 DLVEDWILNNEPASTCTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGNRTTFDPD 120
   |||||
Db 61 DLVEDWILNNEPASTCTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGNRTTFDPD 120
   |||||

Qy 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPIPYPGFDRDLRWRTGKLVPMVCDSSNNFV 180
   |||||
Db 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPIPYPGFDRDLRWRTGKLVPMVCDSSNNFV 180
   |||||

Qy 181 LTKEALEDAYEKAREDNIRVKGILLITNPSNPLGTIMDRKTLRTVVVFINEKRIHLVCDDEI 240
   |||||
Db 181 LTKEALEDAYEKAREDNIRVKGILLITNPSNPLGTIMDRKTLRTVVVFINEKRIHLVCDDEI 240
   |||||

Qy 241 YAAVTFSPQGFISIAEILEDDETDIECDRLNLIHVIVVSLSKDMGFGFRVGIITYSYNDVAVN 300
   |||||
Db 241 YAAVTFSPQGFISIAEILEDDETDIECDRLNLIHVIVVSLSKDMGFGFRVGIITYSYNDVAVN 300
   |||||

Qy 301 CARKMSSFGVLSTQTYQLLASMLNDEFEVERFLAESAKRLAQRFVFTGGGLAKVIGIKCLQ 360
   |||||
Db 301 CARKMSSFGVLSTQTYQLLASMLNDEFEVERFLAESAKRLAQRFVFTGGGLAKVIGIKCLQ 360
   |||||

Qy 361 SNAGLFVWMDLRQLLKPTFSETELKWKVITHEVKINSPGYSFHCTEPGFRVCYANMD 420
   |||||
Db 361 SNAGLFVWMDLRQLLKPTFSETELKWKVITHEVKINSPGYSFHCTEPGFRVCYANMD 420
   |||||

Qy 421 DMVQIALQRIQIRNFVQLNKEVVSNNKKHCWHSNLRSLSKTRRFDITMSPHSPLPQSPMV 480
   |||||
Db 421 DMVQIALQRIQIRNFVQLNKEVVSNNKKHCWHSNLRSLSKTRRFDITMSPHSPLPQSPMV 480
   |||||

Qy 481 KATN 484
   |||||
Db 481 KATN 484
   |||||

RESULT 2
O22464 PRELIMINARY; PRT; 487 AA.
ID O22464
AC O22464;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
GN ACS2.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98340552; PubMed=9675901;
RA Peck S.C., Kende H.;
RT "A gene encoding 1-aminocyclopropane-1-carboxylate (ACC) synthase
RL produces two transcripts: elucidation of a conserved response.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9908479;
RA Peck S.C., Kende H.;
RT "Differential regulation of genes encoding 1-aminocyclopropane-1-
RL carboxylate (ACC) synthase in etiolated pea seedlings: effects of
RL indole-3-acetic acid, wounding, and ethylene.";
RL Plant Mol. Biol. 38:977-982(1998).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AF016459; AAD04199.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 487 AA; 55116 MW; 8485B1DB38497634 CRC64;

Query Match      82.7%; Score 2115.5; DB 10; Length 487;
Best Local Similarity 81.1%; Pred. No. 7.2e-160;
Matches 394; Conservative 47; Mismatches 42; Indels 3; Gaps 2;

Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNFPHFTDNPNGVQMGGLAENQLTS 60
   || |||||
Db 1 MGVMNLDPQLLSKLTAMGDGHEASSYFDGWKAYDKDPFHPKSNPHGVQLQMGGLAENQLTA 60
   || |||||

Qy 61 DLVEDWILNNEPASTCTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGNRTTFDPD 120
   |||||
Db 61 DMVQNWIMSNPEASTCTLEGVHNFKQMANFQDYHGLPEFRNAVAKFMSRTRGNRTTFDPE 120
   |||||

Qy 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPIPYPGFDRDLRWRTGKLVPMVCDSSNNFV 180
   |||||
Db 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPTPYPGFDRDLRWRTGKLVPMVCDSSNNFK 180
   |||||

Qy 181 LTKEALEDAYEKAREDNIRVKGILLITNPSNPLGTIMDRKTLRTVVVFINEKRIHLVCDDEI 240
   |||||
Db 181 LTQKALEAYEKAREDNIRKGLLITNPSNPLGTVMDRNTLTATVTFINEKRIHLISDEI 240
   |||||

Qy 241 YAAVTFSPQGFISIAEILEDDETDIECDRLNLIHVIVVSLSKDMGFGFRVGIITYSYNDVAVN 300
   |||||
Db 241 YAAVTFSPHSFISIAEIIIEHDDETDIECDRLNLIHVIVVSLSKDMGFGFRVGIITYSYNDVVD 300
   |||||

Qy 301 CARKMSSFGVLSTQTYQLLASMLNDEFEVERFLAESAKRLAQRFVFTGGGLAKVIGIKCLQ 360
   |||||
Db 301 CTRKMSFGLVSTQTYQLIAKMLSDDDDFEKEFLPESAKRLAQRYRFTGGLKVGIKCLQ 360
   |||||

Qy 361 SNAGLFVWMDLRQLLKPTFSETELKWKVITHEVKINSPGYSFHCTEPGFRVCYANMD 420
   |||||
Db 361 SNGGLFVWMDLRGLLKPNATFESEIELWRVITHEVKINSPGYSFHCSEBPGFRVCYANMD 420
   |||||

Qy 421 DMVQIALQRIQIRNFVQLQ-NKEVVS--NKKHCWHSNLRSLSKTRRFDITMSPHSPLPPOS 477
   |||||
Db 421 DRDQVIALQIRISFVTQNNKEAMGSKNPKYWHNLRSLSKPRRFDITMSPHSPPIPOS 480
   |||||

Qy 478 PMVKAT 483
   |||||
Db 481 PLVKAT 486
   |||||

RESULT 3
Q9MB64 PRELIMINARY; PRT; 487 AA.
ID Q9MB64
AC Q9MB64;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
GN MDACS-5B.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
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RA Sunako T., Ishikawa R., Senda M., Akada S., Nilzekei M., Harada T.;
RT "MADS-5A (Accession No. AB034992) and 5B (Accession No. AB034993),
RT two wound-responsive genes encoding 1-aminocyclopropane-1-carboxylate
RT synthase in apple. (PGR00-030).";
RL Plant Physiol. 122:620-620(2000).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC -1- ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AB034993; BAA92351.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 487 AA; 54648 MW; D23B9FCB1C68794F CRC64;

Query Match 76.0%; Score 1945; DB 10; Length 487;
Best Local Similarity 73.4%; Pred. No. 2.6e-146;
Matches 359; Conservative 63; Mismatches 59; Indels 8; Gaps 3;

QY 1 MGFKAMQPTLLSKMAIGDGHGESSYFDGKAYDQNPFPHTDNPNGVMQGLAENQLT 60
DB 1 MGFTLSNQOQLLSKATGNGHGENSPYFDGKAYDSDPHTKPNQVGMQGLAENQMC 60
QY 61 DLVEDWILNPNASICTPEGINDFRAIANFQDYHGLAEFRNAVAKEMARTGRNRTFPD 120
DB 61 DLIQEWILNPNASICTAGVNEFKDIAIFQDYHGLPEFRNAVANFMKVGKRNRTFDD 120
QY 121 RIVMSGGATGAHEVTAFAFLADPGAEFLVPIYPYGGFDRLDRLWRTGKLVPMVCDSSN 180
DB 121 RIVMSGGATGAHEMIAFAFLADPGAEFLVPIYPYGGFDRLDRLWRTGKLVPMVCDSSN 180
QY 181 LKAELEADYAKARENIRVKGILLINPSNPLGTIMDRKTLRTVVSFNEKRIHLVCD 240
DB 181 VTAALEAAYEAKAKANIRVKGILLINPSNPLGTIMDRKTLRTVVSFNEKRIHLVCD 240
QY 241 YAATVFSQPGFTSIAELDETDIECDRLNLIHIVYSLSKDMGPGFRVGIYSDAVN 300
DB 241 YAATVFSQPGFTSIAELIEE--NIGNRNLIHIVYSLSKDMGPGFRVGIYSDAVN 298
QY 301 CARKMSSFGLVSTQTOYLLASMLNDDEFERFLAESAKRLAQRFRVFTGGLAKVGIK 360
DB 299 CARKMSSFGLVSTQTOYLLASMLSDNEFVKRFTAQSAKRLKTRMRFTMGLAQVSTN 358
QY 361 SNAGLFWMDRLKLLKPPFDSFTELKWKIIEHVKNVSPGYSFHCTEPGFRVVCYANMD 420
DB 359 SNGGLEFWMDRLRLLEKQTEFAEMVLRWTIIEHVKNVSPGSSFGHCFEPGFRVVC 418
QY 421 DNVAQIALORIRNFVLQNKVEVVVSNKKH-CWHSNRLSLKTRREDD- ----ITMSPH 474
DB 419 DKTMEVALTRITFVLQNKAEIVPRKSNRLWHSNRLSFQSRRDDMTMSPCWMSPH 478
QY 475 PQSPMYKAT 483
DB 479 PQSPLYRAT 487

RESULT 4
P93772 PRELIMINARY; PRT; 489 AA.
AC P93772
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
GN GACS2.
OS Pelargonium hortorum.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Geraniales; Geraniales; Pelargonium.
OX NCBI_TaxID=4031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=88-51-10'; TISSUE=PISTIL;
RX MEDLINE=97435971; PubMed=9290638;
RA Clark D.G., Richards C., Hilloti Z., Lind-Iversen S., Brown K.;
RT "Effect of pollination on accumulation of ACC synthase and ACC oxidase
RT transcripts, ethylene production and flower petal abscission in
RT geranium. (Pelargonium x hortorum L.H. Bailey).";
RL Plant Mol. Biol. 34:855-865(1997).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC -1- ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; U88971; AAB70885.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 489 AA; 55086 MW; 48F71F64B22113D1 CRC64;

Query Match 75.1%; Score 1922; DB 10; Length 489;
Best Local Similarity 73.3%; Pred. No. 1.8e-144;
Matches 354; Conservative 68; Mismatches 53; Indels 8; Gaps 5;

QY 7 DQPTLLSKMAIGDGHGESSYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTSDLVDW 66
DB 9 NQRTLLSKMATGDCGHGENSPYFDGKAYDNNPFLHTQNGVGMQGLAENQSLFIQW 68
QY 67 ILNPNASICTPEGINDFRAIANFQDYHGLAEFRNAVAKEMARTGRNRTFPDRIVMSG 126
DB 69 VLNPQASICTAQGLQEFKDTAIFQDYHGLPEFRNAVANFMKVGKRNRTFPDRIVMSG 128
QY 127 GATGAHEVTAFAFLADPGAEFLVPIYPYGGFDRLDRLWRTGKLVPMVCDSSN 186
DB 129 GATGAHEMIAFAFLADPGAEFLVPIYPYGGFDRLDRLWRTGKLVPMVCDSSN 188
QY 187 EDAYEKAREDNIRVKGILLINPSNPLGTIMDRKTLRTVVSFNEKRIHLVCD 246
DB 189 BEAYERAQEDNIRVKGILLINPSNPLGTILDRTELVSLSVFINENKRIHLVCD 248
QY 247 SQPGFTSIAELDETDIECDRLNLIHIVYSLSKDMGPGFRVGIYSDAVN 306
DB 249 SQPAFVSIAEIVQOE--NVSCNRDLIHIYSLSKDMGPGFRVGIYSDAVN 307
QY 307 SFGLVSTQTOYLLASMLNDDEFERFLAESAKRLAQRFRVFTGGLAKVGIK 366
DB 308 SFGLVSTQTOYLLASMLSDNEFVKRFTAQSAKRLKTRMRFTMGLAQVSTN 367
QY 367 VMDRLKLLKPPFDSFTELKWKIIEHVKNVSPGYSFHCTEPGFRVVCYANMD 426
DB 368 IWDRLRLLEKQTEFAEMVLRWTIIEHVKNVSPGSSFGHCFEPGFRVVC 427
QY 427 ALQIRNFVLQNKVEVV--SNKKHCWHSNRLSLKTRREDDIT--MSPHSP 480
DB 428 ALRRIITFALQNKAEVLPKAIKQCNWNLGRSLSFRRFDDFTMSPHSP 486
QY 481 KAT 483
DB 487 RAT 489

RESULT 5
Q9MB65


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Db 367 DLSRLKQOTFKAEMLWRVVIHEVKLVNVSPPCSFCLKPGWRCVCFANMDDTQMVALS 426
QY 430 RIRNFVLQNKVVVSNKKHCWHSNLRSLKTRFRDITMSPHSPLQSPMVKATN 484
Db 427 RIKTFVNKEADTKSRKNLRWQSLKLLNSPRIYDDFINSPHSPIQSPPLVRARN 481

RESULT 7
Q9FEM2 PRELIMINARY; PRT; 490 AA.
ID Q9FEM2;
AC Q9FEM2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
GN CME-ACS2 (ME-ACS2).
OS Cucumis melo (Muskmelon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3656;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AMS;
RX PubMed=11074269;
RA Ishiki Y., Oda A., Yaegashi Y., Orihara Y., Arai T., Hirabayashi T.,
RA Nakagawa H., Sato T.;
RT *cloning of an auxin-responsive 1-aminocyclopropane-1-carboxylate
RT synthase gene (CME-ACS2) from melon and the expression of ACS genes in
RT etiolated melon seedlings and melon fruits.*;
RL Plant Sci. 159:173-181(2000).
CC -1- CORFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; D86242; BAB18464.1; -.
DR HSP; P37821; I88G.
DR InterPro; IPR001176; ACC-synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 490 AA; 54904 MW; 95754805F958C8FB CRC64;

Query Match 73.3%; Score 1876; DB 10; Length 490;
Best Local Similarity 72.9%; Pred. No. 8e-141;
Matches 347; Conservative 62; Mismatches 63; Indels 4; Gaps 3;

QY 11 LLSKMAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTSDLVEDWILNN 70
Db 15 VLSKLAKNGHGEDSSYFDGWKAYDSDPFPPIINPRGVIOMGLAENQLSFEFEVKMKNN 74
QY 71 PEASICTPGINDFRANFQDYLHGLAEFRNAVAKFWARTGRNRTTDPDRIVMSGGATG 130
Db 75 PQASICSVGEIDFEKDAIFQDYLHGLFEFRNAVANFNGKVRGNRVKFDPPDRVMSGGATG 134
QY 131 AHEVTAFLADPGEAFLVPIPPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 190
Db 135 AHETMAFLADPGEAFLVPPYPPYPGFDRDLRWRTGVEIVPVKCESSNNFKLTREALETAY 194
QY 191 EKAREDNIRKGLLIITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVDEIYAATVFSQPG 250
Db 195 EEAEKSNIRIKGLLIITNPSNPLGTVDYDQTLTAVSFINEKNIHLVDEIYAATVFAEPC 254
QY 251 FTSIAEILEDTEICDRNLVHVIYSLSKDMGPPGFRVGLIYSYNDVAVNCARKMSSFGL 310
Db 255 FISISEVIDMNDVECDRLNIHVYISLSKDMGPPGFRVGLIYSYNDVAVNCARKMSSFGL 314
QY 311 VSTQYQYLLASMLNDDEVERFLAESAKRLAQRFVFTGGLAKVGIKCIQSNAGLFWMD 370

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Db 315 VSSOTQYLIASMLSDVDVDFNFLAGSAEKLAVRRHRTKGLAQVIGYLGSGGGLFLWMD 374
QY 371 LROLLKPTPDSSETELWKVIEHVKINVSFGYSHCTEPGWFRCVYANMDDMAYOIALQR 430
Db 375 LRHLLEKTLAEAWLWKVINEVKLVNVSFGSFSHCSEPGWRCVCFANMDDTMDISITR 434
QY 431 IRNFVLQNKVV--VSNKKHCW-HSNLRSLKTRFRDITMSPHSPLQSPMVKAT 483
Db 435 IRNFVLQNKVVTKVKQKFCWQSSLELRSLSSRLLEDI-MSPHSPLQSPMLRAT 489

RESULT 8
Q9MB85 PRELIMINARY; PRT; 490 AA.
ID Q9MB85;
AC Q9MB85;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
GN CME-ACS2.
OS Cucumis melo (Muskmelon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3656;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ANDES;
RA Shionoi S., Yamamoto M., Inaba A.;
RT *structural characterization of ACC synthase gene from melon and
RT cucumber.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AB032936; BAA93713.1; -.
DR HSP; P37821; I88G.
DR InterPro; IPR001176; ACC-synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 490 AA; 54932 MW; 63B4732473E3F36E CRC64;

Query Match 73.2%; Score 1874; DB 10; Length 490;
Best Local Similarity 72.9%; Pred. No. 1.2e-140;
Matches 347; Conservative 61; Mismatches 64; Indels 4; Gaps 3;

QY 11 LLSKMAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTSDLVEDWILNN 70
Db 15 VLSKLAKNGHGEDSSYFDGWKAYDSDPFPPIINPRGVIOMGLAENQLSFEFEVKMKNN 74
QY 71 PEASICTPGINDFRANFQDYLHGLAEFRNAVAKFWARTGRNRTTDPDRIVMSGGATG 130
Db 75 PQASICSVGEIDFEKDAIFQDYLHGLFEFRNAVANFNGKVRGNRVKFDPPDRVMSGGATG 134
QY 131 AHEVTAFLADPGEAFLVPIPPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 190
Db 135 AHETMAFLADPGEAFLVPPYPPYPGFDRDLRWRTGVEIVPVKCESSNNFKLTREALETAY 194
QY 191 EKAREDNIRKGLLIITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVDEIYAATVFSQPG 250
Db 195 EEAEKSNIRIKGLLIITNPSNPLGTVDYDQTLTAVSFINEKNIHLVDEIYAATVFSQPG 254
QY 251 FTSIAEILEDTEICDRNLVHVIYSLSKDMGPPGFRVGLIYSYNDVAVNCARKMSSFGL 310
Db 255 FISISEVIDMNDVECDRLNIHVYISLSKDMGPPGFRVGLIYSYNDVAVNCARKMSSFGL 314

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Qy	311	VSTQTOYLASMLNDDEFVERFLASAKRAQRFVFTGGGLAKVGKICLQSNAGLFWMD	370
Db	315	VSSOTOYLASMLLDDVFVDNFLAGSAEKLAIVRHRNFTKGLAQVIGVYGLKGGGLFWMD	374
Qy	371	LROLLAKPPTFDSFETELWKVIIIEVKINVSPGYSFHCTEPGHWFCVYKANNDDMAVQIALQR	430
Db	375	LRLLKEKTELEADMAUKWIIIEVKLNVPSPGSGFHCSEPGWFCVYKANNDDSTMDISIR	434
Qy	431	IRNFVLQNKEV--VSNKKHCW-HSNLRSLKTRRFDITMSPHSPLQSPQPMVKAT	483
Db	435	IRNFVLQNKEVTTKVKKQKFCWQRSSLELRLLSRLEDEV-MSPHSPLQSPMLRAT	489
RESULT	9		
Q9S7I1			
ID	Q9S7I1	PRELIMINARY;	PRT; 483 AA.
AC	Q9S7I1;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)		
DE	ACC SYNTHASE.		
GN	ACSI.		
OS	Citrus sinensis (Sweet orange).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid1 II; Sapindales; Rutaceae; Citrus.		
NCBI_TaxId=2711;			
[1]			
SEQUENCE FROM N.A.			
SPRATN-CV. OSBECK.			
Wong W.S., Ning W., Xu P.L., Li N., Yang S.F.;			
"Chilling-inducible ethylene biosynthesis in citrus plant.;"			
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).			
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC			
ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).			
-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT			
CC AMINOTRANSFERASES.			
EMBL; AJ012551; CAB60722.1; -.			
EMBL; AJ012550; CAB60721.1; -.			
HSSP; P37821; 1B8G.			
InterPro; IPR001176; ACC-synthase.			
InterPro; IPR001511; Aminotran_1.			
Pfam; PF00155; aminotran_1.2; 1.			
PRINTS; PR00753; ACCSYNTHASE.			
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.			
Pyridoxal phosphate.			
SEQUENCE 483 AA; 54116 MW; 8BFC37219494085E CRC64;			
Query Match	73.2%;	Score 1873.5;	DB 10; Length 483;
Best Local Similarity	71.3%;	Pred. No. 1.2e-140;	
Matches 345;	Conservative 70;	Mismatches 64;	Indels 5; Gaps
Qy	1	MGFKAMDQTPLLSKMAIGHGESSPYFDGWKAYDONPFPHTDNPNGYQWGLAENQLTS	60
Db	1	MAFALSQNQVLUSKIAANGHGSDSPYFDGWKAFESDPYHPTKPNPVGVIQGLAENLICH	60
Qy	61	DLVEDMLNNEASICTPGINDFRAINFQYHGLAFRNAVAKFMARTGNRTTFDPD	120
Db	61	ELVEDMLNPNKASICSAGELNEFGIALFDQYHGLPEERNVAKFMKVGKRNRTTFDPD	120
Qy	121	RIYVSGGATGAHEVTAFCIADPGAEFLVPIPYPGFDRDLRWRTGKVLVPVWCSSNNFV	180
Db	121	RIYVSGGATGAHEVTAFCIADPGAEFLVPTPYPGFDRDLRWRTGKVLVPVWCSSNDFK	180
Qy	181	LTVEALEADAYEKAREDNIRVKGLITNPSPNPGITMDRKTLTFTVVSFTNEKRIHLVCD	240
Db	181	VTMEALAEAYEKARESNIRKGLITNPSPNPGITMDRKTLDRETLLKDVSVFTNEKRIHLV	240
Qy	241	YAAATVFS-QPGFTISIAEILEDETDIECDRLNVHVIYVLSKOMGPFGRVGIYYSNDAV	299

Db	241	YATVTFKESFVSAIEIDQ--DIACNRNLHIVYLSKDMGFCGFRGIIYSYNDQVV	298
Qy	300	NCARKSSFGVSTQTOYQLASMLNDEFYERELAESAQRKLAQRVFTTGGGLAKVGICL	359
Db	299	SCARKSSFGVSSQTHLTIATWLSDDQFVEKFAIESAKRIABRHKAFTWGLSQVGICL	358
Qy	360	OSNAGLFVMDLQKLLKPPFDSETELWKVIIHEVKINVSFGYSPHCTBPGWFRVCYANM	419
Db	359	KSNAGLFLMDLHLHLKEQYEAEMALRWIIIEVKLNVSFGSFFCNPNGWFRVCYANM	418
Qy	420	DDMAVQIALQIRNFVLQNKVEVVSNNKH-CWHSNLRSLKTRRFDITMSPHSPPLQSP	478
Db	419	DDRTMETALSRIITSEMLKNVEAKVPNNKKLQWRSRLSSSSRRMDDFNASP-CMSQSP	477
Qy	479	MVKA 482	
Db	478	LVQA 481	
RESULT	10		
OB2124			
ID	OB2124	PRELIMINARY; PRT; 489 AA.	
AC	AC2124;		
DT	01-NOV-1998 (TtEMBLrel. 08, Created)		
DT	01-NOV-1998 (TtEMBLrel. 08, Last sequence update)		
DT	01-DEC-2001 (TtEMBLrel. 19, Last annotation update)		
DE	ACC SYNTHASE (1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE).		
GN	CS-ACS2.		
OS	Cucumis sativus (Cucumber).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid1; Cucurbitales; Cucurbitaceae; Cucumis.		
OX	NCBI_TaxID=3659;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=FRUIT;		
RA	Shioml S., Yamamoto M., Ono T., Kakiuchi K., Nakamoto J.,		
RA	Nakatsuka A., Kubo Y., Nakamura R., Inaba A., Imaseki H.;		
RT	"cDNA cloning of ACC synthase and ACC oxidase genes in cucumber fruit		
RT	and their differential expression by wounding and auxin.";		
RN	J. Jpn. Soc. Hort. Sci. 67:685-692(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Shioml S., Yamamoto M., Inaba A.;		
RT	"Structural characterization of ACC synthase gene from melon and		
RT	cucumber.";		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC		
CC	ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT		
CC	AMINOTRANSFERASES		
DR	EMBL; AB006804; BAA33375.1; -;		
DR	EMBL; AB032938; BAA93715.1; -;		
DR	HSSP; P37821; 1B8G.		
DR	InterPro: IPR0011176; ACC_synthase.		
DR	InterPro: IPR001511; Aminotran.1.		
DR	Pfam: PF00155; aminotran_1.2; 1.		
DR	PRINTS; PR00753; ACCSYNTHASE.		
DR	PROSITE; PS00105; AA_TRANSFER.		
KW	Pyridoxal phosphate.		
QY	SEQUENCE 489 AA; 54779 MW; DF140935AIAF5C97 CRG64;		

[illegible]

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QY 71 PEASICTPEGINDPRAIANFQDYHGLAEPRNAVAKFMARTGRNRTITFDDPRIVMSGGATG 130
Db 75 PRASICSVEGIDEFKDIAIFQDYHGLPEFRNAVANFMKVRGRVRFDPDRVVMSSGGATG 134
QY 131 AHEVTAFLCADPGEAFVLPIPPYPGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 190
Db 135 AHEVTAFLCADPGEAFVLPIPPYPGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 194
QY 191 EKAREDIRVKGLLITNPSNPLGTIMDRKTLRTVVSFNEKRIHLVDEIYAATVFSQPG 250
Db 195 EEAQSNIKITKGLLITNPSNPLGTIVDROPLETAVSFINEKRIHLVDEIYAATVFAEPG 254
QY 251 FISIAELEDETIEDCDNLNHLVHIVYSLSKDMGPGFRVGIYIYNDVAVNCARKMSFGL 310
Db 255 FISISEVI-DNSDIECDNLNHLVHIVYSLSKDMGPGFRVGIYIYNDVAVNCARKMSFGL 313
QY 311 VSTOTQYLLASMLNDDFEVERFLAEAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370
Db 314 VSSOTQYLLASMLNDDFEVERFLAEAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 373
QY 371 LROLLKPTFDSDELWKVYIIEHVKINVSFGYSHCTEPGFWFRVCYANMDDMAVQIALQR 430
Db 374 LRLLKPTFDSDELWKVYIIEHVKINVSFGYSHCTEPGFWFRVCYANMDDMAVQIALQR 433
QY 431 IRNFVLQNEKVV--VSNKKHCW--HSNLRSLKTRRFDITMSPHSPLPQSPMVKAT 483
Db 434 IRNFVLQNEKVVTKVKKQKFCWQSSLELRSRRUEDI-MSPHSPLPQSPMHRAT 488

RESULT 11
QY2RC8 PRELIMINARY; PRT; 487 AA.
AC Q2RC8;
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DE 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE ACC SYNTHASE.
OS Carica papaya (Papaya).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Caricaceae; Carica.
OX NCBI_TaxID=3649;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUNSET; TISSUE=30% YELLOW FRUIT;
RA Neupane K.R., Mukatira U.T., Stiles J.I.;
RT "Cloning of Fruit-specific ACC Synthase and ACC Oxidase cDNAs From
RT Papaya (Carica papaya L.) and their Expression During Fruit
RT Ripening.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; U68216; AAC98809.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 487 AA; 55059 MW; 571398012223DA35 CRC64;

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Query Match 71.2%; Score 1823; DB 10; Length 487;
Best Local Similarity 70.9%; Pred. No. 1.3e-136;
Matches 339; Conservative 65; Mismatches 66; Indels 8; Gaps 3;

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QY 11 LLSKMAIGDGHGESSPYFDGKAYDQNPFFHTDNPNGVMQGLAENQLTSDLVEDWILNN 70

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Db 10 LLSKIATSNHGEGSDPYFDGKAYDSDFFHTQNPGEVQMGLEAENQLCFNLHIEWLLKN 69
QY 71 PEASICTPEGINDPRAIANFQDYHGLAEPRNAVAKFMARTGRNRTITFDDPRIVMSGGATG 130
Db 70 PEASICTPAGAAEPDIAIFQDYHGLAEPRNAVAKFMARTGRNRTITFDDPRIVMSGGATG 129
QY 131 AHEVTAFLCADPGEAFVLPIPPYPGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 190
Db 130 AHEVTAFLCADPGEAFVLPIPPYPGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 189
QY 191 EKAREDIRVKGLLITNPSNPLGTIMDRKTLRTVVSFNEKRIHLVDEIYAATVFSQPG 250
Db 190 ETAGEADIKVKGGLIPNPSNPLGTIIYTKDLVLTNNKNIHLVDEIYAATVFSQPE 249
QY 251 FISIAELEDETIEDCDNLNHLVHIVYSLSKDMGPGFRVGIYIYNDVAVNCARKMSFGL 310
Db 250 FTSIAEIIIE-EDKICCNRLDIIHIIYSLSKDMGPGFRVGIYIYNDVAVNCARKMSFGL 308
QY 311 VSTOTQYLLASMLNDDFEVERFLAEAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370
Db 309 VSSOTQYLLASMLNDDFEVERFLAEAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 368
QY 371 LROLLKPTFDSDELWKVYIIEHVKINVSFGYSHCTEPGFWFRVCYANMDDMAVQIALQR 430
Db 369 LRLLKPTFDSDELWKVYIIEHVKINVSFGYSHCTEPGFWFRVCYANMDDMAVQIALQR 428
QY 431 IRNFVLQNEKVVSNKKHCWHSNLRSLKTRRFDIT-----MSPHSPLPQSPMVKAT 482
Db 429 IKTFMLQHKEMVPPKKLQWTSLSLRSFSS-RYEDINETPGSPHSPHSPPIQSPPLVRA 485

RESULT 12
QY2RC8 PRELIMINARY; PRT; 483 AA.
AC Q49904;
DT 01-JUN-1998 (TREMREL. 06, Created)
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE ACC SYNTHASE.
DE ACCS2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Waterings K., Pezzotti M., Cornelissen M., Mariani C.;
RT "Pollination induced ACC-synthase and ACC-oxidase expression.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; X98492; CAA67118.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 483 AA; 54636 MW; C32E7AA38FC2DF0F CRC64;

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Query Match 70.0%; Score 1791.5; DB 10; Length 483;
Best Local Similarity 68.1%; Pred. No. 4.1e-134;
Matches 329; Conservative 79; Mismatches 72; Indels 3; Gaps 3;

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QY 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGKAYDQNPFFHTDNPNGVMQGLAENQLTSD 60

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Db 1 MGFISSIDNELLSKVATNNGHGENSAYFDGKVAEIDPFHTQNSDGVQIOMGLAENQLCF 60
Qy 61 DLVEDWILNPEASTCTPEGINDFRAINFODYHCLAEFRNAVAFKEMARTGCRNRTTFDPD 120
Db 61 DLQIBWVKNPKASICTAEGSODFADIAIYQDYHGLPEFRSAVARFMGKVRGDRITFEPE 120
Qy 121 RIVMSGGATGAHEVTAFCADPGEAFLVPIPIYPGDFDRDLRWRTGKLVPMCDSSNNFV 180
Db 121 RIVMSGGATGAHELLAFCLADPGEAFLVPTYPYPCGDFDRDLRWRTGVLFPVVCSSNNFK 180
Qy 181 LTKALEDAYEKARDNTRVGLLITNPSNPLGTIMDRKTLRTVVVSFINNEKRIHLVCDDEI 240
Db 181 VTKEALEAYKAQESNITVTRGLLNNPSNPLGTILDRLETKDTRVFINNEKRIHLVCDDEI 240
Qy 241 YAAVFSOPGFSTAEILEDETDCDRNLVHIVYSLSKDMGFCGFRVGIISYNDVAVN 300
Db 241 YAAITFNKPFDISISEVIMEE--DVECDRLDHLVYSLSKDLGFGFRVGIISYNDVAVN 299
Qy 301 CARKNSSGLVSTOTQYLLASMLNDEFERFLAESAKRLAQRFRVFTGGLAKVGKICIQ 360
Db 300 CARKNSSGLVSTOTQFLISNMLSDENPVTKFIGESSERLQKRHGMETRGLAQVGINTLK 359
Qy 361 SNAGLFVMDLRQLLKKPTFSETELKWKVITHEVKINVPYSYFCHCTEPGFRVCIYANMD 420
Db 360 SNAGLFVMDLRRLKELTFAELELRIINEVKLNVPSCSFHCSEPGFRVCFANND 419
Qy 421 DMAVQIALQRIRNFVLQNKVVSNKK--HCWHSNLRSLKTRRFDITMSPHPLQSPQSM 479
Db 420 DETMRALRRIRNFVIOQRKGTEGGVKLQCRSKLEISLFRKLDFFMNSPHSPM--SSPL 478
Qy 480 VKA 482
Db 479 VQA 481

RESULT 13

Q941I6 PRELIMINARY; PRT; 485 AA.
ID Q941I6 AC
DT 01-FEB-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ACC SYNTHASE.
GN CM-ACS3.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe T., Fujita H., Sakai S.;
RT *Effects of jasmonic acid and ethylene on the expression of three
RT genes for wound-inducible 1-aminocyclopropane-1-carboxylate synthase
RT in winter squash (Cucurbita maxima).;
RL Plant Sci. 161:67-75(2001).
DR EMBL; AB038559; BAB47124.1; -.
SQ SEQUENCE 485 AA; 54426 MW; 621598080D4EE9E3 CRC64;

Query Match 69.8%; Score 1785.5; DB 10; Length 485;
Best Local Similarity 70.0%; Pred. No. 1.2e-133;
Matches 334; Conservative 67; Mismatches 69; Indels 7; Gaps 5;

Qy 11 LLSKWAIGDGHGESSPYDGNKAYDONPHTDNPNGVQWGLAENQLTSDLVEDWILNN 70
Db 11 LLSKLAINGHGEDSPYDGNKAYDTPDHPHIMNPRGVQIOMGLAENQLSEFEVDWIKNN 70
Qy 71 PEASICTPEGINDFRAINFQDYHGLAEFRNAVAFKEMARTGCRNRTTFDPDRIVMSGGATG 130
Db 71 POASICSVEGLDFKIDIAIFQDYHGLPEFRNAWRILWKGVRGDRVKFDPDRVWMSGGATG 130

Qy 131 AHEVTAFCADPGEAFLVPIPIYPGDFDRDLRWRTGKLVPMCDSSNNFVLTKALEDAY 190
Db 131 AHEVTAFCADPGEAFLVPIPIYPGDFDRDLRWRTGKLVPMCDSSNNFVLTKALEDAY 190
Qy 191 EKARDNTRVGLLITNPSNPLGTIMDRKTLRTVVVSFINNEKRIHLVCDDEIYAATVFSQPG 250
Db 191 EKAQESNIKIKGLLITNPSNPLGTVCROTLETAVAFINQKRIHLVCDDEIYAATVTEPG 250
Qy 251 FTSIAEILEDETDCDRNLVHIVYSLSKDMGFCGFRVGIISYNDVAVNCARKKSSFG 310
Db 251 FTSISEVIENTD--KCDNLHIVYSLSKDMGFCGFRVGIISYNDVAVNCARKKSSFG 308
Qy 311 VSTQYLLASMLNDEFERFLAESAKRLAQRFRVFTGGLAKVGKICIQSNAGLFVMD 370
Db 309 VSSQTHLIASMLSDDEFESFLVGSAKKLAARHNRTRGLAOVGIGYLRGSGGLFLWMD 368
Qy 371 LRQLLKKPTFSETELKWKVITHEVKINVPYSYFCHCT--EPGFRVCIYANMDMAVOIALQ 429
Db 369 LRHLLETKTLEAMALWRVIINDVKAECVAGVVFLLGSPGFRVCFANNDTMEIST 428
Qy 430 RIRNFVLQNKVV--VSNKKHCW--HSNLRSLKTRRFDITMSPHPLQSPQSMVKAT 483
Db 429 RIRNFVLQNKVTTKIKKQKFCROSSLELRSSRLEDI--MSPHPLQSPMLRAT 484

RESULT 14

Q96580 PRELIMINARY; PRT; 483 AA.
ID Q96580 AC
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (EC 4.4.1.14) (ACC
DE SYNTHASE).
GN LE-ACSIB.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. RUTGERS;
RA Oono Y., Nguyen M.D., Hennig L., Yu G., Rottman W.H., Campbell A.D.,
RA Lincoln J.E., Theologis A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 209-311 FROM N.A.
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE = 1-
CC AMINOCYCLOPROPANE-1-CARBOXYLATE + METHYLTHIOADENOSINE.
CC -1- COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; U72390; AAB17279.1; -.
DR HSSP; U74460; AAC49683.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Lyase; Pyridoxal phosphate.
FT VARIANT 43 43 P -> L.
FT VARIANT 139 139 F -> L.
SQ SEQUENCE 483 AA; 54547 MW; 55681096DD7DC2 CRC64;

Query Match

69.6%; Score 1781.5; DB 10; Length 483;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 00:26:04 ; Search time 3456.34 Seconds
(Without alignments)
9660.932 Million cell updates/sec

Title: US-09-763-957-3

Perfect score: 2474

Sequence: 1 ttacagatacacagaatcag.....taaccacatacacatattgg 2474

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_estl.*
10: gb_est2.*
11: gb_hic.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	Length	DB	ID	Description
1	132	5.3	1101	12	CNS00EVL		AL069706 Drosophil
2	130.6	5.3	1101	12	CNS00EVL		AL069706 Drosophil
3	122.2	4.9	1152	10	BG309087		BG309087 HVMC000
4	121	4.9	1101	12	CNS0021J		AL061936 Drosophil
5	119.6	4.8	1101	12	CNS00EVL		AL069440 Drosophil
6	117.4	4.7	1101	12	CNS00EVL		AL069440 Drosophil
7	116	4.7	1101	12	CNS0039G		AL063921 Drosophil
8	114.6	4.6	1101	12	CNS020N7		AL206908 Tetraodon
9	113.2	4.6	1101	12	CNS0021J		AL061936 Drosophil
10	112.8	4.6	1101	12	CNS001T2		AL078714 Drosophil
11	112.6	4.6	1169	12	CNS08KHQ		AL402900 T3 end of
12	110.8	4.5	1101	12	CNS00KZU		AL097152 Drosophil
13	110.4	4.5	994	12	CNS04NOJ		AL298972 Tetraodon
14	110.4	4.5	1101	12	CNS003BD		AL064091 Drosophil
15	110.4	4.5	1161	12	CNS073Y8		AL428118 clone BA0
16	109.6	4.4	1101	12	CNS00B01		AL057419 Drosophil
17	109.6	4.4	1225	12	CNS0161D		AL106171 Drosophil

18	109.4	4.4	994	12	CNS04NOJ	AL298972 Tetraodon
19	109.4	4.4	1101	12	CNS00EVL	AL071206 Drosophil
20	109.4	4.4	1101	12	CNS00KAE	AL077628 Drosophil
21	109.2	4.4	876	12	CNS009G1	AL053529 Drosophil
22	107.2	4.3	889	12	CNS006W4	AL065999 Drosophil
23	106.8	4.3	1101	12	CNS001FB	AL060732 Drosophil
24	106.4	4.3	876	12	CNS009G1	AL053529 Drosophil
25	106.4	4.3	887	10	BF274559	BF274559 GA_Eb002
26	106	4.3	1101	12	CNS00LT2	AL078714 Drosophil
27	106	4.3	1125	9	AL547503	AL547503 AL547503
28	105.4	4.3	889	12	CNS006W4	AL065999 Drosophil
29	105.4	4.3	996	12	CNS00FUH	AL071063 Drosophil
30	105.2	4.3	1161	12	CNS073Y8	AL428118 clone BA0
31	104.8	4.2	781	12	CNS009DO	AL053444 Drosophil
32	104.6	4.2	1101	12	CNS003BD	AL064091 Drosophil
33	104.2	4.2	1101	12	CNS017V2	AL108536 Drosophil
34	103.2	4.2	1125	9	AL547503	AL547503 AL547503
35	103	4.2	905	12	CNS00KHQ	AL077798 Drosophil
36	102.8	4.2	1378	12	AG031694	AG031694 Pan trogl
37	102.6	4.1	1013	12	CNS06RPQ	AL412260 T7 end of
38	102.6	4.1	1190	12	CNS020N7	AL206908 Tetraodon
39	102.2	4.1	734	12	CNS010MP	AL099163 Drosophil
40	102.2	4.1	1225	12	CNS0161D	AL106171 Drosophil
41	102	4.1	1201	12	CNS0167M	AL106396 Drosophil
42	101.8	4.1	769	12	CNS005XX	AL062647 Drosophil
43	101.6	4.1	1200	12	CNS016CO	AL106578 Drosophil
44	101	4.1	1001	12	CNS0155H	AL105023 Drosophil
45	101	4.1	1143	9	AL565457	AL565457 AL565457

ALIGNMENTS

RESULT 1

CNS00EVL

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BAC29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL069706
AL069706.1 GI:4949849
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammeter in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1. .1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"

```

/clone="BACR29B23"
/notes="end : T7"
BASE COUNT 419 a 91 c 60 g 299 t 232 others
ORIGIN

Query Match 5.3%; Score 132; DB 12; Length 1101;
Best Local Similarity 36.5%; Pred. No. 6e-07;
Matches 226; Conservative 129; Mismatches 261; Indels 4; Gaps 1;

Qy 1131 ccactgacgcgctcaacaactcgaattgaattgaagcattgtagtataaggag 1190
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 439 CSCCMWMMHMAATYCTCAHTTMMWMMWMAATTTWMAWMAAATTTATWAAATWAAA 498
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1191 tctagaataattctctaaattctagaggaactatttttaaaaaattcaagaagaagt 1250
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 499 AAWAAMWMAATTTTMMWMTWTTTMMWMTWTTTAAWMAAATAATTTAAW 558
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1251 tctgactataactcttttaaaactttaattctcaacaattttcttatgactcacattgt 1310
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 559 AATAWATTAAWAAATTTAAWAAWTTATTAATTTATTAATTTAAWTTAAATAAAAAATAT 618
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1311 gtgtgaggggtgttctgaataatctctctatttctactagtagtattgtctgcg 1370
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 619 TTTTWTAAATTTTAAATTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 678
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1371 aattatatagtattgaactgtgggaatgattgcctcaataagttataaaaaaggagaaa 1430
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 679 AATTTWAAATTAWAAAAAATAAAAAAATAWAAWAAWATAWAAWTTAAWAAATAAA 738
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1431 atattttactataaaa----aaatacacttaataagtagtaacataataaaaaacattat 1486
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 739 AWAATAATWAAWMAATAATWMAATAATWMAATAATWMAATAATWMAATAATWMAATA 798
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1487 atagagagtaagtaattcaataagtagtgaatgaataaatttttcttctatacaattt 1546
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 799 AWAATAATTAATWAAWMAATAATWMAATAATWMAATAATWMAATAATWMAATAATWMA 858
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1547 gaactaaataattcaataatattcacaagtaataatagatatattcatcattcaataac 1606
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 859 AATATWAAATWAAWAAAAAATAWAAWTTWTTTWWAAWATAATAWAAWATAWAAWAA 918
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1607 gactgaattcaatctattcaatcattatagataaataatacaaatattgtttaaatttt 1666
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 919 AAAAAAATAAATAWMAWMTWATTTWTTTATTAATAAATWTTATWMAWTTWMAWTTWAT 978
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1667 acattattactataataattcaattcttctgaatactctttatatacaagtaggta 1726
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 979 AWTWTATWATATATWTTATWATATATATTTATTAATWATATATTTTAAWAAATAATA 1038
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Qy 1727 gactagaagaattatcttat 1746
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1039 TWATAWMTWATAWAAW 1058

RESULT 2
CNS00EVL/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL069706
VERSION
AL069706.1 GI:4949849
KEYWORDS
GSS.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

```

Db 500 TTTTWTATTAATTTTWTWTWAAATTTWKKK 466

RESULT 3
BG309087/c
LOCUS
DEFINITION
HVSMEC0002A15f 1152 bp mRNA linear EST 22-Oct-2001
HVSMEC0002A15f Hordeum vulgare seedling shoot EST library
HVSMEC0002A15f (Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEC0002A15f, mRNA sequence.
BG309087
BG309087.2 GI:16313791
EST.
SOURCE
ORGANISM
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 1152)
Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling shoot cDNA library
Unpublished (2001)
On Feb 22, 2001 this sequence version replaced gi:13109934.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 119
Seq primer: AATTACCTCCTACTAAGGG
High quality sequence start: 13
High quality sequence stop: 1088.
FEATURES
source
1..1152
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEC0002A15f"
/clone_lib="Hordeum vulgare seedling shoot EST library
HVSMEC0003 (Etiolated and unstressed)"
/tissue_type="Seedling shoot"
/lab_host="TJG121"
/note="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and ceftaxime in covered
crystallization dishes. Five-day old seedling shoots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give pBluescript
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
542 a 31 c 101 g 438 t 40 others

ORIGIN

Query Match 4.9%; Score 122.2; DB 10; Length 1152;
Best Local Similarity 47.0%; Pred. No. 8.3e-06;
Matches 392; Conservative 0; Mismatches 437; Indels 5; Gaps 2;

QY 1203 tcttctaataattagagagaactatttttaaaaaatacaagaaagtgttgatctataac 1362
DB 1115 TTTTTTTTTTTNNAAATGAATTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1056
QY 1263 cttcttaaaccttaaatattctcttgactcacattgtgtgtagaggggtg 1322
DB 1055 TTTTTTTAAATTTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 996
QY 1323 attttgcataatgatgtctatttttatactagtagttgtctgcgaattatataag 1382
DB 995 TAAATTTTATATATATATATTTTNTTTTNTTTTAAATTTTATATTTT--TTATNTTAA 938
QY 1383 tattaacttggagaaatgattgcctaataagttataaaaaaggagaaataattattcat 1442
DB 937 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 878
QY 1443 aaaaaaacacacttaataagtaacaataaaaaaacattataaagagagaaagata 1502
DB 877 AATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 818
QY 1503 atttaataagtagttagaataattttttataataatttgaaactaaaaataattcaa 1562
DB 817 ATATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 761
QY 1563 ataatactcaagtaataatagataataatctcaatcaacgagtagtaattcaatcat 1622
DB 760 TAAATTAATAAATTAATAAATTAATAAATAAATAAATAAATAAATAAATAAATAA 701
QY 1623 tataacataattagataaataacaaattttgttaattttacattattattact 1682
DB 700 TATAAATAATATAAATAATTTTATTAATTTTATTAATTAATTAATTAATTAATTAAT 641
QY 1683 aaatatataattcttcttgaaatcttttatacaagtaggtagactagaagaattatc 1742
DB 640 AAATTTTATTTTATTAATTTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 581
QY 1743 ttatctccgataattgttagatggttaaatgtaacgggcttagactgagttttgtatt 1802
DB 580 AAATTTAATTTNTAATAAATTTTNTTTTTTTTTTTTAAATAATTAATTAATTTTNTT 521
QY 1803 atattattataaacattagagatttaagtttaagtctctctcttgatttttaacatggt 1862
DB 520 TTTTNTTT 461
QY 1863 tctaaaaattaggttttaataatcgtctcaatgaacccatgctatatttttaagtt 1922
DB 460 NTTT 401
QY 1923 tttgttttttgacaattgttttttttttttttttttttttttttttttttttttttt 1982
DB 400 TTTTATTTGGGGTGTGGGGGTTTGTGTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 341
QY 1983 gatactagaaacgaagagtagagtagtgatagtagtgatagtagtgatagtagtgatag 2036
DB 340 ATTTGTTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 287

RESULT 4
CNS0021J/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL061936
VERSION AL061936.1 GI:4940214
KEYWORDS
GSS.

BASE COUNT

[illegible]

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	source
Location/Qualifiers	1..1101
/organism="Drosophila melanogaster"	
/db_xref="taxon:7227"	
/clone_lib="RPCI-98"	
/clone="BACR05N11"	
/note="end : TET3"	

BASE COUNT 631 a 7 c 28 g 289 t 146 others
ORIGIN

Query Match 4.6%; Score 113.2; DB 12; Length 1101;
Best Local Similarity 43.5%; Pred. No. 9.6e-05;
Matches 330; Conservative 62; Mismatches 355; Indels 12; Gaps 3;

QY 1408 ataagttataaaaggagagaatatttatttcataaaaaaacacacttaaatagtaa 1467
|| || || || || || || || || || || || || || || || || || || || ||
Db 341 AA 400

QY 1468 caataataaaaaccattatatagaagattaagataatttaagtagtgattgtagat 1527
|| || || || || || || || || || || || || || || || || || || || ||
Db 401 AA 460

QY 1528 aattttattcataaatttgactaaaattccaaataattcceaagtaaatatagat 1587
|| || || || || || || || || || || || || || || || || || || || ||
Db 461 AA 520

QY 1598 ataattcatctcaatcacgagttaattccaatctattataatcatatagataaata 1647
|| || || || || || || || || || || || || || || || || || || || ||
Db 521 TTAWTTTTTTTAAATTAATTTTTTTTTTTTTTTTTTTTTTTTAAATTTTAAWNAWA 580

QY 1648 caaatattgttaacatttatattactataatataattctcttcctgaata 1707
|| || || || || || || || || || || || || || || || || || || || ||
Db 581 AATTATAAANAANWTWTTAATTTAAATTAATTAANAANAANAANWTTTAAANWTWT 640

QY 1708 tottttacagtaggtagactagaagaattctcttctcccgatatatttgt----a 1762
|| || || || || || || || || || || || || || || || || || || || ||
Db 641 TTTTWTAAATTAATAAANAANAATATAAATTTTATTTAAATTAATTTTAAAAA 700

QY 1763 gatgttaaatgaacggcctagactgatgtttttgttattattattataaatccatt 1822
|| || || || || || || || || || || || || || || || || || || || ||
Db 701 WTTTTTTAAATTTTTTTTAAAATTTTAAATTTTAAATTTTAAANWTAAATTTT 760

QY 1823 agagatttaagtt---aattgcctctcttgattttaacatggtctcaaaagtaggttt 1878
|| || || || || || || || || || || || || || || || || || || || ||
Db 761 AAATTAATTAATTAANAANAATTTTAAATTTTAAATTTTAAATTTTAAAAA 820

QY 1879 aatcattgcgtctccaatgaaccccatgctatattgttttaagttttttgttttgacaa 1938
|| || || || || || || || || || || || || || || || || || || || ||
Db 821 AAAAAATAAAAAATAAAAAAANAANAANAANAANAANAANAANAANAANAANA 880

QY 1939 tgttttttattctcgagat---tgctcttaggattggaattatgtttgatcactagaaac 1995
|| || || || || || || || || || || || || || || || || || || || ||
Db 881 TTTTAATAATGATTTAAATGTGTTTTTAAAGTTAAANAANAATGKAATGGKKGKTARKK 940

QY 1996 gaagaagtagagagtagtgcataacgctgtgtaaaaaataatagttgtggagacttaagttg 2055
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Db 941 GRGCTTAARAATDGTGAACAKKATAAKKTKTKTAAYKKTAANAADKAKGAAATAATWGAA 1000

QY 2056 gatttgaatactaggacgaggtggaagggtttccactaagttgacaaaattattacaa 2115
|| || || || || || || || || || || || || || || || || || || || ||
Db 1001 GKATGAAAAGTGKDAATATTTKKNAANAANAANAANAANAANAANAANAANA 1060

QY 2116 gtggcaactagctagggtctcacaagtagtattactaattaa 2154
|| || || || || || || || || || || || || || || || || || || || ||
Db 1061 RAAKAAADAADAKAGAGTGTDDAADATATWTKGKTCTKTA 1099

RESULT 10
CNS00LT2
LOCUS CNS00LT2 1101 bp DNA linear GSS 14-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:

COMMENT: Determination of this BAC-end sequence was carried out as part of a

SOURCE
ORGANISM
Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 994)
Roest-Crolius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 994)
Roest-Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
3 (bases 1 to 994)
Genoscope.
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>.
Location/Qualifiers
1..994
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone_lib="122P04"
/clone_lib="G"
/note="Genoscope sequence ID : COBG122DH02LP1-end : T7"
BASE COUNT 543 a 49 c 36 g 194 t 172 others
ORIGIN

Query Match 4.5%; Score 110.4; DB 12; Length 994;
Best Local Similarity 40.3%; Pred. No. 0.00021;
Matches 327; Conservative 53; Mismatches 429; Indels 2; Gaps 1;

QY 1153 tcacaatgtaataagaagcattgtagtataagaagagctagaataaaattcttcaata 1212
DB 972 TCATAATAAAATTTAATAACAATTTAAATTAATTTTAAAAATATATTTTACAA 913
QY 1213 ttagaggaaaactatttttaaaaaatacaagaagagtttgatctataaccctttaaac 1272
DB 912 AAAATTTATATTTTATATTAATTAATTTATTTTAAATTAATTAATTAATTAATTA 853
QY 1273 tttaaatattcaacaattttcttgactcacatctggttgtaggggtatttgtcaa 1332
DB 852 AVAATATATATTTTATTTTAAATTAATTAATTAATTTTAAATTAATTTTAAATTA 793
QY 1333 aatatatgtctattatactagtagtattgctgcgaattatataatagataacttg 1392
DB 792 TATTTATATATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 733
QY 1393 gagaatgatgctgaatgataaaaaagagagaaatattattatcataaaaaaata 1452
DB 732 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAAATTA 673
QY 1453 cacttaataagtaacaataataaaaaacattataagagattaagaataatttaag 1512
DB 672 TAATWATATAATANTATTTATATATAAATAAATAATATATTTATTTTAAATTA 613
QY 1513 tattgaatgagaataaattttattataaatttgactaaaaataattcaataattca 1572
DB 612 TTTTATATATTTTATATATTAATTAATTTTATTTTATTTTATTTTATTTATTA 553
QY 1573 aegtaataatagataataatcatcatcattcaatcagagattccaattcattataatcata 1632

Db 552 TNATTAAATATAMWATTTTTTTTTTTTAT--NNTTATTATATATATATTTTTTATWTTTATNATA 495
QY 1633 tattagataaatacaaaaattattgttaaaattttacattattattactaaaaataatat 1692
Db 494 TATAAAT 435
QY 1693 taattcttttgatatactttttacaaagtaggtagacagaagaattctctctcccg 1752
Db 434 WATTWATATAAAATWTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 375
QY 1753 tatatttgtagattgtaaaatgaacggcctagactgattttttgtattatattatta 1812
Db 374 WTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 315
QY 1813 taatccattagagatttaagtaagtcctctctttgatttaacatggtctctaaaaatt 1872
Db 314 BTTSNNBTNNNNNNNTGTTTWTTCCTCATTTCTGCATGGGCGTGTSMWTM 255
QY 1873 aggttaatactatgctgcctcaaatgaacccatgctatatttttaaaagtgtttttttt 1932
Db 254 TTTTMTGTTGTTGGMTTMTTKCMNMTSMSTTSTTMTMTKTSMTMTSTCMMTMTTMTT 195
QY 1933 tgacaagtgttt 1963
Db 194 MGMTTMTTTCMTATATTTTTCMGMTTSMWT 164
RESULT 14
CNS003BD/C
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K08 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL064091
VERSION AL064091.1 GI:4941847
KEYWORDS
SOURCE fruit fly.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammos in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K08"
/note="end : TET3"
BASE COUNT 395 a 120 c 103 g 334 t 149 others
ORIGIN

FEATURES
source

Db 666 AAAAAATTTTAAATTTATTAATAAATTAATAATTTAAATATAATATTTNTTAAATTAAT 725
QY 1587 tataattcatcattcaatcagagtaattccaatctctataataatcataatattagataaataat 1646
Db 726 ATTTTAAATAAATTTTAAATTAATTAATTAATAATAATAATAATAATAATAATAATAATA 785
QY 1647 acaaatatttgtaaatatttacattattataataataataataataataataataataata 1706
Db 786 ATAAGTTATATATATAATAATTAATAATAATAATAATAATAATAATAATAATAATAATA 845
QY 1707 atcttttatacaagtaggtagactagaagaattatctctcccgctattcttgtagatg 1766
Db 846 ATNATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 905
QY 1767 ttaaatgtaacggcttagactgatgtttttgtatttatattataataatccattagag 1826
Db 906 TATGTTTT-----TTATATAGATTTTTTTTTTTTTTTTTTTTTTTTATTTTATTTAGAT 958
QY 1827 atttaagtttaagtct 1886
Db 959 WGGTAA---TAAGAGTKTNATTTGTTTTTGAATTTDNGAKTTTTTTTTTTTTTTTATTTT 1015
QY 1887 cgtccccaatgaaccatgctatatgttttaaaagttttttgttttttttttttttttttt 1946
Db 1016 TTKKTTTATTTGTTTGTGTTTWKATRAAATTTTAGATTTAKTTAKTTGCGWAAATTTATTTT 1075
QY 1947 atttctgagatgctctcttaggattgaaattatgttt 1982
Db 1076 TTTTTTTTTTTTWT 1111

Search completed: August 21, 2002, 00:26:31
Job time: 5682 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 01:59:05 ; Search time 96.17 Seconds
(without alignments)
6318.990 Million cell updates/sec

Title: US-09-763-957-3
Perfect score: 2474
Sequence: 1 ttacagatcacagaatcag.....taaccacataccatcatgg 2474

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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5: /cgn2.6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91.4	3.7	1511	1	US-07-991-867B-8
2	91.4	3.7	1511	1	US-08-107-755A-8
3	91.4	3.7	1511	2	US-08-544-332-8
C 4	88.6	3.6	636	4	US-08-998-416-1137
C 5	88.2	3.6	837	4	US-08-998-416-288
C 6	88.2	3.6	19124	2	US-08-487-826B-13
C 7	87.6	3.5	8920	2	US-08-446-855A-1
C 8	87.6	3.5	8920	4	US-09-150-741-1
C 9	84.2	3.4	19124	2	US-08-487-826B-13
C 10	83.4	3.4	615	4	US-08-998-416-186
C 11	81.6	3.3	636	4	US-08-998-416-1137
C 12	80	3.2	615	4	US-08-998-416-186
C 13	79.8	3.2	837	4	US-08-998-416-288
C 14	79.2	3.2	51952	3	US-08-947-823-1
C 15	78.8	3.2	665	2	US-08-883-795A-36
C 16	78.6	3.2	6243	2	US-09-056-075-1
C 17	77.4	3.1	665	2	US-08-883-795A-36
C 18	74.4	3.0	6124	4	US-08-213-419B-3
C 19	74	3.0	658	4	US-08-998-416-595
C 20	73.4	3.0	1431	4	US-09-316-083-2
C 21	73	3.0	3701	4	US-08-845-258-10
C 22	73	3.0	3701	4	US-08-990-571-10
C 23	73	3.0	3701	4	US-08-723-142A-10
C 24	72.8	2.9	6152	4	US-08-973-462-1
C 25	72.6	2.9	1431	4	US-09-316-083-2
C 26	72.6	2.9	7218	1	US-08-232-463-14
C 27	72.4	2.9	660	1	US-07-991-867B-32

28	72.4	2.9	660	1	US-08-107-755A-32	Sequence 32, Appl
29	72.4	2.9	660	2	US-08-544-332-32	Sequence 32, Appl
30	72.4	2.9	4810	3	US-08-852-629-11	Sequence 11, Appl
31	72.4	2.9	4838	3	US-08-852-629-15	Sequence 15, Appl
C 32	71.6	2.9	6124	4	US-08-213-419B-3	Sequence 3, Appl1
C 33	71.4	2.9	834	4	US-08-998-416-305	Sequence 305, App
C 34	70.4	2.8	658	4	US-08-998-416-595	Sequence 595, App
C 35	70	2.8	828	4	US-08-998-416-538	Sequence 538, App
C 36	70	2.8	6243	2	US-09-056-075-1	Sequence 1, Appl1
C 37	69.8	2.8	854	4	US-08-998-416-534	Sequence 534, App
C 38	69.2	2.8	5852	1	US-07-867-106-2	Sequence 2, Appl1
C 39	68.8	2.8	2430	4	US-08-845-258-3	Sequence 3, Appl1
C 40	68.8	2.8	2430	4	US-08-845-258-40	Sequence 40, Appl
C 41	68.8	2.8	2430	4	US-08-990-571-3	Sequence 3, Appl1
C 42	68.8	2.8	2430	4	US-08-990-571-40	Sequence 40, Appl
C 43	68.8	2.8	2430	4	US-08-723-142A-3	Sequence 3, Appl1
C 44	68.8	2.8	2430	4	US-08-723-142A-40	Sequence 40, Appl
C 45	68.6	2.8	834	4	US-08-998-416-305	Sequence 305, App

ALIGNMENTS

RESULT 1
US-07-991-867B-8
; Sequence 8, Application US/07991867B
; Patent No. 5476781
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
; TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/991,867B
; FILING DATE: 12-DEC-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 92/14818
; FILING DATE: 12-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,685
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/657,584
; FILING DATE: 19-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF114.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1511 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:


```

; NAME/KEY: CDS
; LOCATION: complement (234..782)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 852..1511
US-08-107-755A-8

Query Match      3.7%; Score 91.4; DB 1; Length 1511;
Best Local Similarity 44.8%; Pred. No. 9e-09;
Matches 501; Conservative 0; Mismatches 596; Indels 22; Gaps

QY 665 tataccaattaattatttctttaaatttgacatttgacttcttataataaacaattatg 724
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Db 71 TATATTATTTGATAATTCGTTATTAAATCGTTATTGATATTAAACAATATTATTATCA 130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 725 tatggattgaatcgatatcggtgacaattgaagtttccctcaagtttagccattttat 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 TTTTACCATTATTTTTTTTTTCTATCTACTACGAAATATCAGATTTTGCACCTTCAATAT 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 785 gaattaaacttaactactactattaggtaaatcatctatgtatcattaaacaattcoagt 844
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 191 CAGAATAAATAATTATCATTTA-TTTTGCATTTATGAATAAAAATATTAAATATGAATTATTA 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 845 tgagttcaaattttaccocaagatttgaaagttgtgtcaactctgttaactaaagtctga 904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 TAACAATAATCTACACACAGAAACATATAAATCTTGTCCACCATTTTCAATTTATTGTGATTT 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 905 ttaagagttgacgacttttaa-----cctaaatctatttgaattgaaggggtt 953
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 TTATTATGTTTTTAAATCTGTAAGAAGCAGTCCTTTTATACAAAATTGACATATAGCTTTGT 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 954 gatgacttcagcttttaaaaataattcaactaaagttctctagactacatctggagatttagtg 1013
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 AATTTTTTTTATTTTTTCTACTTTAGGAATTAAATTTTGATATTAGAAATTAAATATATTTCTG 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1014 ttcataaaatttttagaaaaaggtgagtttaaagtttatgaaaaagattggtgactattcaa 1073
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 TTAAGCTCAAAATTTAATCCAGCAACAATAAATCTTTTTTTTTTTTATTATTAGCCATTTTATCA 489
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1074 ttaattagttggaattgatgcacaaattttcatgagcataaccaatcagagaaatacca 1133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 490 CAAAAATGTTCTAAATCAATTTCTTCAAAAATTTGCACTCATCTATGCCCAATAAATATCA 549
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1134 cctcgaccgactacaacaactctcaatgttaattgaatgaagcattgtagtaagaagctct 1193
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 550 TAATTTATCTACGATATTGTATTCATTAATTAAATTTATTTGTTTAAATGTATAAATATCT 609
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1194 agaataaaattcttaaatatagaggaacactatttttcaaaaaattacaagaaaaagtttg 1253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 610 TTATTTTAAATATATTTCCGTCATGATTTATATATTTTTTTTATTATAAATCTATATCTATA 669
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1254 atctaaacctctttaacctttaaattatctaaacatttcttatgactcacattggtt 1313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 670 TTATGAGTTATTAATTACACATTTTGTATAGATAAAATATATCTATTAATTTTTCGCATC 729
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1314 gataggtgattttgtcaaaaatatgtctattttatactagtagtattgtgtctgcgaat 1373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 730 AATTCGTGTTTTCGCCAAGAACATAGG-----ACCAATTTAATTCATCTCGA 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1374 tatatagatttaacttggagaatgatgtcctaataagttaataaaaaaggagaaaaata 1433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 780 CATTTTTTTTTTATTATTGATATATTTTCAAAAAAAAATTAATCAATGAAAAAAAAT 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1434 ttctatcataaaaaaaatacaccttaaaataagtaacaaataataaaaaacattataaagag 1493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 840 AAAATTTATCAAAATGGATTTTACTAAATTTCTGATATAATTTTAAATAATTTTAAATAAT 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1494 attaagataatttaataagctattgagttagaataatttttattataaaatttgaactaa 1553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 900 TATATTTTAAAAAATAATAATAAACACAGAGATATGTATTAAATATTAATATATTAAAA 959
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1554 aatattcaaaataataatcaagaagtaataatagataataattcatcatcacaacagtaaat 1613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Query Match 3.5%; Score 87.6; DB 4; Length 8920;
Best Local Similarity 44.7%; Pred. No. 5.5e-08;
Matches 482; Conservative 0; Mismatches 579; Indels 17; Gaps 3;
Qy 639 atttaatggaggattttttttccatataccaattatttttttaattttatgcatt 698

Db 918 ATTTTATTTTATATATATATACATTTTCATACATTTTCACACACATTTAA 977
QY 1283 ctaacaattttcttgactcacattgt---gttgatagggtgatttctgcaaaatatat 1339
Db 978 GTTGTCATAATGTAACACATTAATAATATATATATATATATATATATATATATAT 1037
QY 1340 gtctattttactagtagatttctgcgaattatataatagatttaacttggagaat 1399
Db 1038 ATATTAAATAAAATATTTATCGCTGTTATATATATATATATATATATATATATAT 1097
QY 1400 gattgcctaagtctataaaaggagaaaattatttctcataaaaaaacacacttaa 1459
Db 1098 CTTCAAAAT 1157
QY 1460 ataagtaacaataaaaaaacattataagaagataaagataatttaagtagttgaa 1519
Db 1158 ATGTTATGTAATGCAATTAATAAGATAAAATCTATAGCTATATATATATATATAT 1217
QY 1520 tbtagaataattttttattataaaatttgaactaaaaatttcaa-----ataatattcaa 1573
Db 1218 TAT 1277
QY 1574 agtaataatagataaattcattcattcaatcagagaaattcaactctattataa----- 1627
Db 1278 ATTTTAAATAATATATTTGTATACATACAGACTAAGAAACTATACATCTGGTA 1337
QY 1628 --tcataatagataaaatacaaatatttggtaaaattttacattattataatacaaa 1685
Db 1338 TCFAATAGTAT 1397
QY 1686 tatataatatttcttggatattcttttatacaagtaggtagactagaagaattactta 1745
Db 1398 TAAATAATAAATAAT 1457
QY 1746 tctcccgatattttagatgttcaaatgttaacgggcttagactgatttcttattata 1805
Db 1458 ATAAATAATCTTTTAAAAACCTTCAAAACATTTTTCATATAAATAATATATATATAGT 1517
QY 1806 ttattataaattccatagagatttaagt 1834
Db 1518 AACCACTAGATAAATAGAGAAACGT 1546

RESULT 10
US-08-998-416-186/c
; Sequence 186, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416

; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1074RP
; US-08-998-416-186

Query Match 3.4%; Score 83.4; DB 4; Length 615;
Best Local Similarity 49.7%; Pred. No. 2.4e-07;
Matches 239; Conservative 0; Mismatches 241; Indels 1; Gaps 1;
QY 1416 ataaaaaggagaaaattatttattcataaaaaaacacattcaataagcaacaataa 1475
Db 583 ATAAATGATAAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 524
QY 1476 aaaaacattatacaagagatttaagataaatttaagtagtttgaatgtagaattttta 1535
Db 523 ATATAATTTTATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 464
QY 1536 ttataaaatttgaaacataaatttcaataaatttcaaaagataaataagataataattca 1595
Db 463 AATAAATATCTTTTAAAAAGTTAAATAATAATAATAATAATAATAATAATAATAATA 404
QY 1596 tcattcaatacagagtaattcaattcattataatcaatataattagataataacaaatt 1655
Db 403 TATTATAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 344
QY 1656 tgttaaatatttaccattattataatacaataataataatttcttgaatattttttat 1715
Db 343 ATATATATTTTAAATAACAAATTAATAATAATAATAATAATAATAATAATAATAATA 284
QY 1716 acaagtaggtagactagaagaatttcttattctcccgatatattttagatgttaaatga 1775
Db 283 AATTTATTAAGAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 225
QY 1776 acgggcttagactgattgttttattattattattattataatccattagagatttaagt 1835
Db 224 ACATAGACTAAATAGTATTCATATTAATAATAATAATAATAATAATAATAATAATAATA 165
QY 1836 aatgtctctcttggatttttaacatggttctcaaaaattaggtttcaatcgcctcctca 1895
Db 164 TGATGAATTAAGTAAATTTATATAATAATAATAATAATAATAATAATAATAATAATA 105
QY 1896 t 1896
Db 104 T 104

RESULT 11
US-08-998-416-1137
; Sequence 1137, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine

```

; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgene
; APPLICANT: Knechtie, Philipp
; APPLICANT: Reblschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPYII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 1137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1692RP
; US-08-998-416-1137

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Query Match 3.3%; Score 81.6; DB 4; Length 636;
Best Local Similarity 50.8%; Pred. No. 5.1e-07;
Matches 301; Conservative 0; Mismatches 279; Indels 12; Gaps 4;

Qy 1410 taagttataaaaggagaaataattttattcattataaaataacacttaataagtaaca 1469
Db 20 TAAATTTAAAGATTAATATAACCTTTTATTATAATATTAAAGTATTAAATTTAA 79

Qy 1470 ataataaaacattataagagattaaagtaatttaataagattagaaagataaa 1529
Db 80 ACTATTATTATCATATTATAAATTA--ATTATTGATTATTAACTATTATTATAAA 137

Qy 1530 tttttattataaatttgaaactaaataattcacaataattcacaagtaaaataagatat 1589
Db 138 TATTATATATAATTACITTAATTCATCATATTATTAATATTATATAATTAATAATAATAT 197

Qy 1590 aatcacaattcaatagagaaatcaatcattattataatcattattagataaataaca 1649
Db 198 TTAATATG----ATACTATTATTAGTCTATGTTCAAAATTTTAAATTAGTATTATAAATATT 253

Qy 1650 aattttgttaaatattacattatattactataatattataattcttctgaatc 1709
Db 254 ATTAGATATTATTATTTCTTTTAATAAATATTAAATAGATTATCAATAATTAATATTATT 313

Qy 1710 ttttatacaagtagtagacagaagaattattcttctccgtagatttttgtagatgta 1769
Db 314 ATTTTATAA---TTGTTTATTAAAAATAATATTTTATTATTATAAAGATTAAATTTATT 370

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Qy 1770 aatgaacgggcttagactgatgttttttgattattattattataaaatccatcattagagatt 1829
Db 371 TAAATATTGTAATATTATTATTATTATAATAATCTATTATTATAAATATTATGTTGATT 430

Qy 1830 taagttaattgtctctctttgatttttaacatgggttctaaaaaattaggttttaacattgcgt 1889
Db 431 TATATTATTAAATCTTTT---TATAAGAAATTATTATAAATTAATTTTAACTTTAAATTT 487

Qy 1890 cctcaatgaacccatgctatatgtttttaaagtttttttgatttttttgacaatgttttttatt 1949
Db 488 CTTATTATTATTATTATTATTATTATAAATTAATATATATTCATTTTATTATTATTATTATT 547

Qy 1950 tctgagattgctcttagagattgaaattatgttttgatactagaaaacaaagaa 2001
Db 548 AATTAATAATTATTATTAAATTAATTTTATTCATTTATTATTAAATTAATTAATAA 599

RESULT 12
US-08-998-416-186
; Sequence 186, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgene
; APPLICANT: Knechtie, Philipp
; APPLICANT: Reblschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPYII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1074RP
; US-08-998-416-186

```

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Query Match 3.2%; Score 80; DB 4; Length 615;
Best Local Similarity 49.7%; Pred. No. 9.9e-07;
Matches 294; Conservative 0; Mismatches 285; Indels 13; Gaps 3;

```

[illegible]

: PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: CH 0016/97
 : FILING DATE: 31-DEC-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Meigs, J. Timothy
 : REGISTRATION NUMBER: 38, 241
 : REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1376
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 919-541-8587
 : TELEFAX: 919-541-8689
 : INFORMATION FOR SEQ ID NO: 288:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 837 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : ORIGINAL SOURCE:
 : ORGANISM: PAG1241RP
 : US-08-998-416-288

	Query Match	3.2%	Score 79.8;	DB 4;	Length 837;
	Best Local Similarity	49.9%;	Pred. No. 1.1e-06;		
	Matches	313;	Conservative	0;	Mismatches 302; Indels 12; Gaps 4;
QY	1410	taagttataaaaggagaaaaata	ttttattcataaaaaaacacacttaaat	aagtaaca	1469
DB	20	TAAATTTAAAGATTAATAA	TAACCTTTTTTATTATAATATT	TAAAGTATTAATTTATT	79
QY	1470	ataataaaacattataaagagat	caagtaatttaataaagtattgaatg	agaataa	1529
DB	80	ACTATTATTATCATATTATT	TAATAAAATTA--ATTATTTGATT	ATTAAATCATTATTATATAA	137
QY	1530	ttttattataaatttgaactaaaa	tattcaataataattccaaagtaaat	atagatat	1589
DB	138	TTATTATATAATTACTTAAT	TATCATATTATAATTTATATAAT	TATAAAATAATAT	197
QY	1590	aattcatcattcaatacagagta	aattcaactattataaatcatata	tattagataaataca	1649
DB	198	TTAATATG---AATACATATT	TAGTCATGTCAAATTTTAAAT	TAGTTATTAAAAATATT	253
QY	1650	aattttgttataaattcacattat	tattactaaaaataattaaattctt	tttgaatc	1709
DB	254	ATTAGATATTATTATTTTCTT	TATAAATTTATTAATATAGATT	ATCAATTAATTAATATT	313
QY	1710	ttttacaagtagtgagactaga	gaattatctctccgtatatattgt	agatgta	1769
DB	314	ATTATTAA---TTGTTTATT	AAAAATAATATATTTATTATT	TATAAAGATTAAATTT	370
QY	1770	aatgtaacggcttagactgatg	ttttgtattatatattataaact	cattagagatt	1829
DB	371	TAAATATTGTAAATATTATT	TTTATTATATAATCTATTTT	TATAAATAATATCTTGATT	430
QY	1830	taagttaatgctctcttga	tttttaacatggttctaaaaat	taggttttaacatcgct	1889
DB	431	TATATTATTAACTTTTT---	TATAGAAATATTATTAAAA	TAAATTTTAACTTTAATTT	487
QY	1890	cctcaatgaaccatgctatg	tttcaagttttttgtttttt	gttgacaaagtgtttt	1949
DB	488	CTTATTATTAAATTTTATAT	TATTAAATTAATATATTTT	TCATTTTATTATTATTATT	547
QY	1950	tctgagattgctcttaggatt	gaattatgtttgtactagaaa	cgaagtagag	2009
DB	548	TAAPTAAATTAATTTATT	TAAATTTTATCATTTTAA	TATTAAATTAATAATATTA	607
QY	2010	tagtgatacacgctgtaaaaa	taata	2036	
DB	608	TAAAGAATGTAGTTAAAA	AATCTTATA	634	

RESULT 14
US-08-947-823-1

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RESULT 13
US-08-998-416-288
; Sequence 288, Application US/08998416
; Patent NO. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebeschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NO. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435

```


ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Michelle
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: ORGANISM: Homo sapiens
IMMEDIATE SOURCE: CLONE: Rh 32
US-08-883-795A-36

Query Match 3.2%; Score 78.8; DB 2; Length 665;

Best Local Similarity 48.6%; Pred. No. 1.7e-06;
Matches 246; Conservative 0; Mismatches 257; Indels 3; Gaps 1;

QY 1428 aaataatttattcataaaaaaacacttaataagtagaacaataaaaaaacattata 1487
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DB 47 AAAATATTTATAATTAATAATTTATATAATTAATAATTTTATAATTAATAATTTATAAAT 106
QY 1488 taagagattaaagataatttaataagtagatgaatgagaataattttttattataaatttg 1547
|||
DB 107 AAATATTTTATAATTAATAATTTTATAATTAATAATTTTATAATTAATAATTTTATAAAT 166
QY 1548 aactaaataattcacaataattcagaagtaataataagataataattcattcattcaatcag 1607
|||
DB 167 AAATATTTTATAATTAATAATTTTATAATTAATAATTTTATAATTAATAATTTTATAAAT 226
QY 1608 agtaattcaatctattataatcatattagataaaataacaaatatttgtaaatttta 1667
|||
DB 227 AAATATTTTATAATTAATAATTTTATAATTAATAATTTTATAATTAATAATTTTATAAAT 286
QY 1668 cattattatattactaataatattattcttttgaaatctcttttatacaagtaggtag 1727
|||
DB 287 AAATATTTTATAATTAATAATTTTATAATTAATAATTTTATAATTAATAATTTTATAAAT 346
QY 1728 actagaagaattatctctcccgtagatttgtagattgtaaatgtaacgggcttagac 1787
|||
DB 347 ACATATTTTATAATTAATAATTTTATAATTAATAATTTTATAATTAATAATTTTATAAAT 406
QY 1788 tgatgtttttgtattattattttaaaatcca---ttagagattttaagtttaagtctct 1844
|||
DB 407 ACATATTTTATAATTAATAATTTTATAATTAATAATTTTATAATTAATAATTTTATAAAG 466
QY 1845 ctttgatttaacatgggtcttaaaaattaggtttaatcatcttgctcctcaatgaacccat 1904
|||
DB 467 TATTTATAATTAACATATTTTATAATTAATAATTTTATAATTAATAATTTTATAAATTAAG 526
QY 1905 gctatatgttttaaaagttttttgttt 1930

Db 527 TATTATAATTACATATTTTATAAATTT 552

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Job time: 9412 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 02:07:21 ; Search time 477.34 Seconds
(without alignments)
8898.576 Million cell updates/sec

Title: US-09-763-957-3
Perfect score: 2474
Sequence: 1 ttacagatacacagaatcag.....taaccacatacacatattgg 2474

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits.satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.*
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15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1994.DAT.*
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17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	2474	100.0	2474	21	AAZ94266	
2	119.2	4.8	15548	24	ABL341155	
3	110.4	4.5	6106	22	AAS46429	
4	110.4	4.5	6106	24	ABL33472	
5	109.4	4.4	6175	24	ABL33307	
c	6	108.2	4.4	8169	22	AAS46287
7	104.8	4.2	11996	24	ABL34493	
c	8	103.4	4.2	700	22	AAH93026
c	9	102.8	4.2	1864	8	AAH71405

10	102.8	4.2	6092	24	AA561080	Human gene regulat	
11	102.8	4.2	10048	24	AA561252	Human gene regulat	
12	101.4	4.1	700	22	AAH93026	Human inflammatory	
13	101	4.1	12393	24	ABL33263	Human immune syste	
14	100.6	4.1	7676	24	ABL34598	Human metastasis a	
15	99.8	4.0	6123	24	ABL32821	Human immune syste	
16	99.2	4.0	15548	24	ABL34155	Human immune syste	
c	17	99	4.0	5992	24	AA561208	Human gene regulat
18	99	4.0	7461	24	ABL33784	Human immune syste	
19	98.4	4.0	19787	24	ABL33451	Human immune syste	
20	97.8	4.0	5979	22	AA545313	Chemically pretrea	
21	97.6	3.9	8305	24	ABL33569	Human immune syste	
c	22	97.6	3.9	18624	24	ABL33702	Human immune syste
23	97.4	3.9	6071	24	ABL32325	Human immune syste	
24	97.4	3.9	6071	24	AA561076	Human gene regulat	
25	97.2	3.9	8246	24	ABL32202	Human immune syste	
c	26	96.8	3.9	4590	7	AAH60472	Sequence encoding
27	96.6	3.9	17280	22	AA546771	Tumour suppressor	
28	96.6	3.9	18624	24	ABL33702	Human immune syste	
29	96.4	3.9	5413	22	AA546694	Tumour suppressor	
c	30	96.4	3.9	5641	24	ABL33397	Human immune syste
31	96.4	3.9	13584	24	ABL32615	Human immune syste	
c	32	96.2	3.9	7597	24	ABL33013	Human immune syste
33	96.2	3.9	15732	22	AA545388	Chemically pretrea	
34	95.4	3.9	61020	22	AA546788	Tumour suppressor	
c	35	95.2	3.8	14919	22	AA546506	Tumour suppressor
36	95	3.8	9810	24	ABL32427	Human immune syste	
37	94.8	3.8	5748	24	ABL33143	Human immune syste	
c	38	94.8	3.8	6106	22	AA546429	Tumour suppressor
c	39	94.8	3.8	6106	24	ABL33472	Human immune syste
40	94.8	3.8	9155	24	ABL32463	Human immune syste	
41	94.6	3.8	8310	20	AAZ29911	CDNA encoding a SC	
42	94.2	3.8	5999	24	ABL32853	Human immune syste	
c	43	93.8	3.8	18218	24	ABL33949	Human immune syste
c	44	93.6	3.8	6641	24	ABL32315	Human immune syste
45	93.4	3.8	6131	24	ABL32890	Human immune syste	

ALIGNMENTS

RESULT 1
AAZ94266
ID AAZ94266 standard; DNA; 2474 BP.
AC AAZ94266;
DT 03-JUL-2000 (first entry)
XX Mung bean ACC synthase AIM-1 gene promoter pGEL-1.
DE Mung bean; 1-aminocyclopropane-1-carboxylic acid synthase;
KW ACC synthase; AIM-1; promoter; pGEL-1; transgenic plant; ds.
XX Vigna radiata.
XX WO200012714-A1.
XX 09-MAR-2000.
XX 31-AUG-1999; 99WO-AU00705.
XX 31-AUG-1998; 98AU-0005572.
XX (UYUQ) UNIV QUEENSLAND.
XX Botella Mesa JR, Cazzonelli CI;
XX WPI; 2000-270821/23.
XX Isolated nucleic acid molecule for producing transgenic plants having
PT altered characteristics such as resistance to a plant pathogen
PT comprises promoter, inducible in response to physical stimulation -

XX Claim 5; Fig 4i-ii; lllpp; English.
 PS The present sequence is that of the promoter, termed pGEL-1, of the
 CC mung bean 1-aminocyclopropane-1-carboxylic acid synthase gene, AIM-1.
 CC AIM-1 was identified as a mechanical strain-induced gene, and the
 CC promoter was cloned using a long distance inversion PCR procedure.
 CC pGEL-1 is capable of induction by physical and/or environmental
 CC stimuli in cells in which it is indigenous and, in the absence of
 CC any negative regulatory mechanism, is capable of constitutive
 CC expression in cells in which it is non-indigenous. The invention
 CC relates to this promoter, and also to derivatives of the promoter
 CC including modular forms which are, for example, inducible by
 CC different physical and environmental stimuli or which are
 CC constitutively expressed. The promoter can be used to direct
 CC expression of genes conferring useful traits on plants, such as
 CC improved resistance to a plant pathogen, altered nutritional
 CC characteristics, expression of a plantabody, altered biochemical
 CC pathway, altered fertility, and/or altered flower colour.
 XX
 SQ Sequence 2474 BP; 844 A; 372 C; 363 G; 895 T; 0 other;

Query Match 100.0%; Score 2474; DB 21; Length 2474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ttacagatcacagaatcagacacacatctacttttaataacagaaaaataaagtgtc 60
 Db 1 ttacagatcacagaatcagacacacatctacttttaataacagaaaaataaagtgtc 60

Qy 61 ggagattatggtacagacaagaatgaaatgtttttatatgttggtgagattatttggctgtt 120
 Db 61 ggagattatggtacagacaagaatgaaatgtttttatatgttggtgagattatttggctgtt 120

Qy 121 gttggaagtttcagaatcatgatttgattttacgtattacgtattaaaaatgaaagtgaatc 180
 Db 121 gttggaagtttcagaatcagatcgaatttgattttacgtattaaaaatgaaagtgaatc 180

Qy 181 atgcattttatctagaagctgggaactgaacccaaaaaaatagccagttggaacactgcag 240
 Db 181 atgcattttatctagaagctgggaactgaacccaaaaaaatagccagttggaacactgcag 240

Qy 241 tattttaggcgtattatctctcttccctacacataatccttggctgtcttttatcgga 300
 Db 241 tattttaggcgtattatctctcttccctacacataatccttggctgtcttttatcgga 300

Qy 301 aaaaaacaaaagaacatagctactctgtaaggtcctcgattgccgacaagaacatcacat 360
 Db 301 aaaaaacaaaagaacatagctactctgtaaggtcctcgattgccgacaagaacatcacat 360

Qy 361 gcgtgctgcgaagaacacataaatttggaggttgaagctcagtcgagttttgcattt 420
 Db 361 gcgtgctgcgaagaacacataaatttggaggttgaagctcagtcgagttttgcattt 420

Qy 421 ttttaggttatgtgtacacgtatgagtgagttccgcgtatatagtgtaggtagtgagtg 480
 Db 421 ttttaggttatgtgtacacgtatgagtgagttccgcgtatatagtgtaggtagtgagtg 480

Qy 481 gctgagtagcgagtgaaatcaggttaacactatcttttcaagccacctaattaaaggattta 540
 Db 481 gctgagtagcgagtgaaatcaggttaacactatcttttcaagccacctaattaaaggattta 540

Qy 541 atgttcatgcgaactgtttcttcgtaactaaggcccccacttaccctttataattctctct 600
 Db 541 atgttcatgcgaactgtttcttcgtaactaaggcccccacttaccctttataattctctct 600

Qy 601 aactccgggcttttggtaagtcacaactttttctactcttatttaattgaggagattatttt 660
 Db 601 aactccgggcttttggtaagtcacaactttttctactcttatttaattgaggagattatttt 660

Qy 661 tccatataccaataaatttttttaattttatgcattttgattcttatataaacaatt 720
 Db 661 tccatataccaataaatttttttaattttatgcattttgattcttatataaacaatt 720

Db 661 tccatataccaataaatttttttaattttatgcattttgatctttattataaacaatt 720

Qy 721 atggtatgagtaagtcgtatatacggtgacaatggaagtttccccaagtttagccatt 780
 Db 721 atggtatgagtaagtcgtatatacggtgacaatggaagtttccccaagtttagccatt 780

Qy 781 ttatgaattataaacttaactactactatttaggttaaatcatatgtatcattaaacaatttc 840
 Db 781 ttatgaattataaacttaactactactatttaggttaaatcatatgtatcattaaacaatttc 840

Qy 841 aatgtgaattcaattttccccaagaatttgaagttgttgaacttctgttaactaaagt 900
 Db 841 aatgtgaattcaattttccccaagaatttgaagttgttgaacttctgttaactaaagt 900

Qy 901 tgtattcaaggttgacgaccttaacctaactattttgaattgaagggtttagtgact 960
 Db 901 tgtattcaaggttgacgaccttaacctaactattttgaattgaagggtttagtgact 960

Qy 961 tcagcttttaaaataaattccaactaaagtctctagactacatttgagatttttagttcataa 1020
 Db 961 tcagcttttaaaataaattccaactaaagtctctagactacatttgagatttttagttcataa 1020

Qy 1021 aattttgaaaaaaggctgagttanaagttatgaaaaaaggattggtagctattcaattata 1080
 Db 1021 aattttgaaaaaaggctgagttanaagttatgaaaaaaggattggtagctattcaattata 1080

Qy 1081 gttgtgaattgatgacaaatatttcatgagcataccaactcagagaataaccactcgac 1140
 Db 1081 gttgtgaattgatgacaaatatttcatgagcataccaactcagagaataaccactcgac 1140

Qy 1141 cgactacaacaatctcaatgtttaatttaagaagcattgtagtataaaggagttctagaataa 1200
 Db 1141 cgactacaacaatctcaatgtttaatttaagaagcattgtagtataaaggagttctagaataa 1200

Qy 1201 atttcttaaatatttagaggaataactatttttaaaaaataaccagaagaaagtttgactata 1260
 Db 1201 atttcttaaatatttagaggaataactatttttaaaaaataaccagaagaaagtttgactata 1260

Qy 1261 accttttaaaacttttaaatattcttaacaaattttctttagctcacattgtgttgatagg 1320
 Db 1261 accttttaaaacttttaaatattcttaacaaattttctttagctcacattgtgttgatagg 1320

Qy 1321 tgattttgcataataatatactatttttatactagcatagttgtcctgcgaattatataat 1380
 Db 1321 tgattttgcataataatatactatttttatactagcatagttgtcctgcgaattatataat 1380

Qy 1381 agtattcaacttggagaataatgctcctaagttataaaaaagagaaaaattatttttc 1440
 Db 1381 agtattcaacttggagaataatgctcctaagttataaaaaagagaaaaattatttttc 1440

Qy 1441 ataaaaaaaatacacacttaataaagtaacaataataaaaaacattataaagagattaaga 1500
 Db 1441 ataaaaaaaatacacacttaataaagtaacaataataaaaaacattataaagagattaaga 1500

Qy 1501 taatttaataagttatgaaatagaaataattttttattataaaatttgaactaaataattc 1560
 Db 1501 taatttaataagttatgaaatagaaataattttttattataaaatttgaactaaataattc 1560

Qy 1561 aataaataatccaagtaataatagataataatcattcatcattcaatcagagtaattcaatct 1620
 Db 1561 aataaataatccaagtaataatagataataatcattcatcattcaatcagagtaattcaatct 1620

Qy 1621 attataatcatattattagataaataacaaaatttttgaattttacattattattata 1680
 Db 1621 attataatcatattattagataaataacaaaatttttgaattttacattattattata 1680

Qy 1681 ctataataatattatttttttgaataatctttttacaaagtaggtagactagaagaatta 1740
 Db 1681 ctataataatattatttttttgaataatctttttacaaagtaggtagactagaagaatta 1740

Qy 1741 tcttatctcccggtattattttagatggttaaatgttaacgggcttagactgagtgtttttgta 1800
 Db 1741 tcttatctcccggtattattttagatggttaaatgttaacgggcttagactgagtgtttttgta 1800

[illegible][illegible]

Db	10810	atttagtataataatcattatacaataataattattatacaattttaagaaatttagttat	10869
Qy	1509	taegtattgaattagataaattttttattataaatttgaactaaaattccaataata	1568
Db	10870	ataataataattataat-ttaagaattataacgtataattataatttaataatta	10928
Qy	1569	tccaagtaanaataagataataatcaatcattcaatcgcggaattcaactattataat	1628
Db	10929	tataatcgtataataattataataatgt----aatattataattattata	10984
Qy	1629	catattagataaataatacaaaatcttctcaaaatttcatattattattactaaatat	1688
Db	10985	atagtaataattatattataataatacaattattataataataatacaattat	11044
Qy	1689	atattaattcttttgaatatctttatacaagtaggtagactagaagaattattctatct	1748
Db	11045	attataataataataataattatattataataataataattattataataatt	11104
Qy	1749	cccgatatatttgttagagtggttaaaagtaacgggcttagactgagtcttttgtattatata	1808
Db	11105	ataatatattagtaataatttttttgacggagttttatttttatgttttaggttgag	11164
Qy	1809	ttataaatccattagagatttaagttaagtctctctcttggatttttaacatgggtctaaa	1868
Db	11165	tttaatggtgcgaatttcgatttattgtcatttttcatttttgggttcaagtgatttttt	11224
Qy	1869	aattagggttaaatcatcgcgtcccaatgaaccatgctatctatttttaagtttttgt	1928
Db	11225	gttttagttttcgcgtaagttgggattatagggtatttgatcatcgtatcggttaatttt	11284
Qy	1929	tttttgacaatgttttttattttctcgagattgctcttaggatt	1970
Db	11285	ttttttttttttttttttgtatttttagtagagagatggatt	11326

RESULT 8

AAH93026/c
ID AAH93026 standard: DNA: 700 BP.

AC AAH93026;

DT 09-OCT-2001 (first entry)

Human inflammatory bowel disease related gene fragment IGR3319a.

Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; KW
single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; KW
chromosome 5q31-33; forensic test; gene therapy; ds. KW

OS Homo sapiens.

AA
PN
WO200142511-A2.

14-JUN-2001.

11-DEC-2000: 2000WO-US33632.

XX 10-DEC-1999: 99US-0170257.

PR 10-APR-2000; 2000US-0196046.
XX

PA (WHEE) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX	Daly M.	Hudson T.J.	Lander ES.	Rioux
PI				

XX
DR WPI: 2001-367874/38.

PT Testing for the presence of polymorphisms associated with inflammatory
AA bowel disease, using a hybridization assay -

PS Disclosure: Page 384: 463pp: English.

XX

The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a gene containing a polymorphic site described in the exemplification of the invention.

Sequence 700 BP; 370 A; 13 C; 14 G; 302 T; 1 other;

Query Match	4.28;	Score 103.4;	DB 22;
Best Local Similarity	50.5%;	Pred. No. 2.1e-06;	
Matches 307; Conservative		0; Mismatches 292;	Indels 9; Gaps 2

Qy	1273	tttaaatattcatcaaaaattttcttatgactcacattgttgtagtaggggtgatttggctcaa	1332
Db	676	TTAAATATATTAAATATATATTAAATATATATATATATATATTTTAAATATAATNTAAATAATAA	617
Qy	1333	aatatatgtctattttacactagatgatgttgcgcgaattcatatatagatttaacttgc	1392
Db	616	ANTATATATTATATATTTAAATATATATATATATATATTTTAAATATATATATTAATATATAT	557
Qy	1393	gagaaaatgatgcctcaacagttcaaaaaagggagaaaatatcttattctcaaaaaaaaata	1452
Db	556	TATATATATTTAAAAATATATATATATATATTTAAACATATTTTAAANATATATATTTAAAAAATA	497
Qy	1453	cacttaaaatagtaacaataataaaaaacattatataagagagattaaagatacaatttaasg	1512
Db	496	TAAATTTATATATTATATATAATATATATATATATATATATATATAATATAATATATATAA	437
Qy	1513	tattgaatgtagaataaattttatttataaaattgacataaaatattcgaataaattc	1572
Db	436	TATATAATTTATAT	377
Qy	1573	aagtaaaataatagatatataatcattccatcacgagtaattcaatctattataatcat	1632
Db	376	ATTGTATATTTATATATTTGTATATATTTATATATATATATATATATATATATATTTTATATAT	317
Qy	1633	tattagataaaataca-----aatattgttaaaattttcacatttatattactaa	1684
Db	316	ATATATATTTATATATATATATATATATTTTATATATATATTTTATATATATATATATTTAT	257
Qy	1685	atatattaactttcttgaatatcttttatacaagtaggtgagactagaaga-attatct	1743
Db	256	ATATATTTTTATATATTTTTATATATTTTATATATATATATATATATTTTATATATATATAT	197
Qy	1744	tatctccggtatatattgttagatgtttaaagtgaacggccttagactgagtcttttgcatta	1803
Db	196	ATATTTATATATATATTTTAT	137
Qy	1804	tattcttataaaatccattagagatttaagttcaatgtctctcttgcatttttaacatggct	1863
Db	136	TTTTTATATATTTTTTATATATTTTACATATATATATTTTTTATATATTTTTTATATATATATAT	77
Qy	1864	ctaaaaat	1871
Db	76	TTATATAT	69

RESULT 9

AAN71405/C

ID AAN71405 standard; DNA; 1864 BP.

AC AAN71405;

DT 18-APR-19

Sequence of ANS-1 which in

Enzyme: fungal expression vector: *Aspergillus* expression vec

kw Enzyme; target expression vector; Aspergillus expression vector;

renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds: tumour; immunostimulant; cardiact; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.

XX
OS Homo sapiens.

XX
PN W0200177375-A2

FN 100-200-2001
XX
100-200-2001

PD 18-OCT-2001.
XX

PF 06-APR-2001;
XX

PR 06-APR-2000;
PR 07-APR-2000;

PR 30-JUN-2000;

PR 01-SEP-2000; 2000DE-104
XX

PA (EPIG-) EPIGENOMICS AG.
XX

PI Olek A, Piepenbrock C,
XX

DR WPI; 2002-017470/02.

xx PT New nucleic acid sequences from chemically modified genes associated
PT with gene regulation, useful for analysing cytosine methylations for
PT diagnosis and therapy of diseases e.g. severe combined immunodeficiency
PT disease -

XX
SD
Claim 1. See ID No. 26. See: Serial

The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preecampsta, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic

CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 6092 BP; 1931 A; 122 C; 1140 G; 2899 T; 0 other;

Query Match	4.2%	Score 102.8;	DB 24;	Length 6092;
Best Local Similarity	44.2%;	Pred. No. 2.2e-06;		
Matches 610; Conservative	0;	Mismatches 757;	Indels 13;	Gaps 4;

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